

FIG. 4A-1

Gene	NCBI Accession Number	FOLD INCREASE
glyceraldehyde-3-phosphate dehydrogenase	M33197	23.02
ribosomal protein L29	NM_000992	21.62
heat shock 90kD protein 1, beta	A1218219	21.27
Lysosomal-associated multispinning membrane protein-5	NM_006762	20.19
ferritin, light polypeptide	BG538564	19.50
Consensus includes gb:AJ249377.1 /DEF=Homo sapiens partial mRNA for human Ig lambda light chain variable region, clone MB91 (331 bp). /FEA=mRNA /GEN=IGLV /PROD=immunoglobulin lambda variable region /DB_XREF=gi:5911837 /UG=Hs.247898 Human anti-streptococ	AJ249377	18.95
Consensus includes gb:D84143.1 /DEF=Human immunoglobulin (mAb59) light chain V region mRNA, partial sequence. /FEA=mRNA /PROD=immunoglobulin light chain V-J region /DB_XREF=gi:1255613 /UG=Hs.121508 Human immunoglobulin (mAb59) light chain V region mRNA,	D84143	18.76
gb:AJ225092.1 /DEF=Homo sapiens mRNA for single-chain antibody, complete cds. /FEA=CDS /PROD=immunoglobulin /DB_XREF=gi:3090425 /UG=Hs.249245 Homo sapiens mRNA for single-chain antibody, complete cds /FL=gb:AJ225092.1	AJ225092	18.62
ribosomal protein L29	BF683426	18.53
Consensus includes gb:L48784 /DEF=050 Homo sapiens cDNA /FEA=mRNA /DB_XREF=gi:1066715 /UG=Hs.182426 ribosomal protein S2	L48784	17.74
profilin 1	NM_005022	17.74
ornithine decarboxylase antizyme 1	AF090094	16.18
serine hydroxymethyltransferase 2 (mitochondrial)	NM_005412	15.75
chaperonin containing TCP1, subunit 7 (eta)	NM_006429	15.12
ribosomal protein L8	NM_000973	14.94
macrophage migration inhibitory factor (glycosylation-inhibiting factor)	NM_002415	14.75
Consensus includes gb:D84140.1 /DEF=Human immunoglobulin (mAb56) light chain V region mRNA, partial sequence. /FEA=mRNA /PROD=immunoglobulin light chain V-J region /DB_XREF=gi:1255610 /UG=Hs.248043 Human immunoglobulin (mAb56) light chain V region mRNA,	D84140	14.48
transketolase (Wernicke-Korsakoff syndrome)	BF696840	14.41
ribosomal protein L18	NM_000979	14.38
transketolase (Wernicke-Korsakoff syndrome)	L12711	13.75
ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	AA910614	12.75
glyceraldehyde-3-phosphate dehydrogenase	M33197	12.69
glyceraldehyde-3-phosphate dehydrogenase	BF689355	12.67
nuclease sensitive element binding protein 1	BE966374	12.57

FIG. 4A-2

neutrophil cytosolic factor 4 (40kD)	NM_013416	12.52
T-cell leukemia/lymphoma 1A	X82240	12.46
ribosomal protein L18a	NM_000980	12.33
glyceraldehyde-3-phosphate dehydrogenase	BE561479	12.29
gb:L07950.1 /DEF=Homo sapiens MHC class I HLA B71 mRNA, complete cds. /FEA=CDS /GEN=HLA-B /PROD=MHC HLA B71 /DB_XREF=gi:307236 /FL=gb:L07950.1	L07950	12.26
ubiquitin carrier protein	NM_014501	12.12
actin, beta	X00351	11.85
enolase 1, (alpha)	U88968	11.53
replication factor C (activator 1) 2 (40kD)	M87338	11.48
phosphoserine aminotransferase	NM_021154	10.95
MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	AF279900	10.74
ribosomal protein S5	NM_001009	10.69
RNA polymerase II transcriptional regulation mediator (Med6, S. cerevisiae, homolog of)	NM_005466	10.68
eukaryotic translation initiation factor 3, subunit 8 (110kD)	BC000533	10.65
chaperonin containing TCP1, subunit 2 (beta)	AL545982	10.52
CGI-135 protein	NM_016068	10.35
polymerase (DNA directed), delta 2, regulatory subunit (50kD)	NM_006230	10.25
ribosomal protein L13	AW574664	9.93
procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	J02783	9.85
HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae)	NM_001536	9.83
cold inducible RNA binding protein	NM_001280	9.66
ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit	BE798517	9.57
pinin, desmosome associated protein	AF112222	9.50
pyruvate kinase, muscle	NM_002654	9.43
gb:L23516.1 /DEF=Human Ig rearranged gamma-chain, V-DXP4-JH6c, complete cds. /FEA=mRNA /DB_XREF=gi:385218 /FL=gb:L23516.1	L23516	9.42
fusion, derived from t(12;16) malignant liposarcoma	NM_004960	9.37
immunoglobulin heavy constant mu	U80139	9.32
maternal G10 transcript	NM_003910	9.30
major histocompatibility complex, class I, B	D83043	9.29
small EDRK-rich factor 2	NM_005770	9.29
heat shock 90kD protein 1, beta	AF275719	9.05
Consensus includes gb:AF254822 /DEF=Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced /FEA=CDS_2 /DB_XREF=gi:10946127 /UG=Hs.78202 SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, memb	AF254822	8.88
protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	NM_002707	8.77
glucose phosphate isomerase	NM_000175	8.76
proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	NM_002812	8.74

FIG. 4A-3

ribosomal protein S19	BE259729	8.68
eukaryotic translation elongation factor 1 alpha 1	AL035687	8.48
gb:L23518.1 /DEF=Human Ig rearranged gamma-chain, V-DXP1-JH4b, complete cds. /FEA=mRNA /DB_XREF=gi:385220 /FL=gb:L23518.1	L23518	8.41
ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit	NM_001687	8.41
procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	NM_000918	8.38
endothelial differentiation-related factor 1	AB002282	8.37
acid phosphatase 1, soluble	BG035989	8.33
chaperonin containing TCP1, subunit 3 (gamma)	NM_005998	8.32
proteasome (prosome, macropain) subunit, alpha type, 7	AL078633	8.23
Consensus includes gb:AF043584.1 /DEF=Homo sapiens clone ASMneg1-b1 immunoglobulin lambda chain VJ region, (IGL) mRNA, partial cds. /FEA=mRNA /GEN=IGL /PROD=immunoglobulin lambda chain /DB_XREF=gi:2865479 /UG=Hs.287815 Homo sapiens clone ASMneg1-b1 immu	AF043584	8.21
non-POU-domain-containing, octamer-binding	L14599	8.09
CGI-51 protein	NM_015380	8.07
adaptor-related protein complex 2, mu 1 subunit	NM_004068	7.95
interferon regulatory factor 4	NM_002460	7.90
ribosomal protein S19	NM_001022	7.90
interferon stimulated gene (20kD)	NM_002201	7.88
dolichyl-diphosphooligosaccharide-protein glycosyltransferase	D29643	7.80
actin, beta	X00351	7.72
major histocompatibility complex, class II, DR alpha	M60333	7.69
major histocompatibility complex, class I, B	L42024	7.62
major histocompatibility complex, class II, DR beta 5	AJ297586	7.57
actin, gamma 1	AL567820	7.49
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 3 (9kD, B9)	NM_004542	7.48
HLA-B associated transcript 1	NM_004640	7.47
ribosomal protein L18a	AC004692	7.36
H2A histone family, member O	AI313324	7.31
gb:U62824.1 /DEF=Homo sapiens HLA class I heavy chain (HLA-Cw*1701) mRNA, complete cds. /FEA=CDS /GEN=HLA-Cw*1701 /PROD=HLA class I heavy chain /DB_XREF=gi:1575443 /UG=Hs.287811 H.sapiens mRNA for HLA-C alpha chain (Cw*1701) /FL=gb:U62824.1	U62824	7.31
major histocompatibility complex, class II, DR alpha	M60334	7.27
ribosomal protein S15	NM_001018	7.26
eukaryotic translation initiation factor 3, subunit 8 (110kD)	NM_003752	7.25
U6 snRNA-associated Sm-like protein LSm7	NM_016199	7.25
eukaryotic translation elongation factor 2	NM_001961	7.22
membrane-spanning 4-domains, subfamily A, member 1	X12530	7.13
eukaryotic translation initiation factor 3, subunit 8 (110kD)	AA679705	7.11

FIG. 4A-4

spermidine synthase	NM_003132	7.09
polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	BG335629	7.09
ribosomal protein S2	NM_002952	7.03
chemokine (C-X-C motif), receptor 4 (fusin)	AF348491	7.03
RNA, U2 small nuclear	BC003629	7.00
similar to HYPOTHETICAL 34.0 KDA PROTEIN ZK795.3 IN CHROMOSOME IV	BE747342	6.98
origin recognition complex, subunit 5-like (yeast)	AF081459	6.94
DEAD-box protein abstrakt	NM_016222	6.93
immunoglobulin heavy constant mu	BC001872	6.90
DKFZP564M182 protein	AK000822	6.88
nuclear RNA helicase, DECD variant of DEAD box family	NM_005804	6.86
stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	BE886580	6.80
immunoglobulin heavy constant mu	BG340548	6.76
mutS homolog 6 (E. coli)	D89646	6.75
tubulin, beta, 4	AL565749	6.75
major histocompatibility complex, class II, DR beta 1	U65585	6.73
T cell receptor beta locus	M15564	6.72
major histocompatibility complex, class II, DP alpha 1	M27487	6.62
ribonucleotide reductase M1 polypeptide	AI692974	6.62
signal sequence receptor, delta (translocon-associated protein delta)	NM_006280	6.59
seryl-tRNA synthetase	NM_006513	6.55
eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)	NM_001415	6.54
protein phosphatase 1, regulatory subunit 7	BF718769	6.52
ancient ubiquitous protein 1	NM_012103	6.52
glutathione S-transferase pi	NM_000852	6.49
polymerase (RNA) III (DNA directed) polypeptide K (12.3 kDa)	NM_016310	6.42
ubiquinol-cytochrome c reductase core protein I	NM_003365	6.42
proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	AB033605	6.41
splicing factor, arginine/serine-rich 5	AW084582	6.40
SKB1 homolog (S. pombe)	NM_006109	6.32
cell death-regulatory protein GRIM19	NM_015965	6.20
U6 snRNA-associated Sm-like protein	NM_012321	6.18
eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)	U36764	6.17
mitochondrial ribosomal protein S2	NM_016034	6.17
D123 gene product	NM_006023	6.16
replication factor C (activator 1) 2 (40kD)	NM_002914	6.15
membrane-spanning 4-domains, subfamily A, member 1	BC002807	6.09
Rab acceptor 1 (prenylated)	NM_006423	6.02
eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)	BC001173	5.97
ubiquitin C	M26880	5.97
valosin-containing protein	AF100752	5.94
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	AL080089	5.93
CD22 antigen	X52785	5.93

FIG. 4A-5

B lymphoid tyrosine kinase	NM_001715	5.89
mitochondrial ribosomal protein S34	NM_023936	5.88
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1)	NM_005004	5.88
mitochondrial ribosomal protein L9	AB049636	5.86
ribosomal protein S2	AI183766	5.85
actin binding LIM protein 1	NM_006720	5.84
syntaxin 16	AK026970	5.84
major histocompatibility complex, class II, DR beta 4	NM_021983	5.83
protein kinase, DNA-activated, catalytic polypeptide	U34994	5.82
ribosomal protein S28	AC005011	5.81
eukaryotic translation initiation factor 4A, isoform 1	NM_001416	5.80
ribosomal protein, large, P0	BC003655	5.76
NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	AF155235	5.76
ATP citrate lyase	U18197	5.75
Consensus includes gb:BF979419 /FEA=EST /DB_XREF=gi:12346634 /DB_XREF=est:602288246F1 /CLONE=IMAGE:4373914 /UG=Hs.119122 ribosomal protein L13a	BF979419	5.74
glutaminyl-tRNA synthetase	NM_005051	5.74
Consensus includes gb:AF005487.1 /DEF=Homo sapiens MHC class II antigen (DRB6) mRNA, HLA-DRB6*0201 allele, sequence. /FEA=mRNA /DB_XREF=gi:5915893 /UG=Hs.167385 Homo sapiens MHC class II antigen HLA-DRB6 mRNA, partial cds	AF005487	5.73
eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)	NM_003751	5.71
polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)	BC005903	5.70
mitochondrial ribosomal protein S12	NM_021107	5.66
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	NM_004889	5.66
putative human HLA class II associated protein I	BE560202	5.65
hypothetical protein	NM_016459	5.64
membrane component, chromosome 11, surface marker 1	BG258784	5.58
hypothetical protein PRO1847	AF119855	5.57
proteasome (prosome, macropain) subunit, beta type, 7	NM_002799	5.57
cell division cycle 2-like 2	AF067524	5.57
similar to RIKEN cDNA 2310040G17 gene	BF972185	5.57
putative transmembrane protein; homolog of yeast Golgi membrane protein Yif1p (Yip1p-interacting factor)	NM_020470	5.57
tryptophanyl-tRNA synthetase	M61715	5.56
ribosomal protein, large, P0	NM_001002	5.56
transcription factor Dp-1	NM_007111	5.55
guanine nucleotide binding protein (G protein), beta polypeptide 1	AI741124	5.54
actin, gamma 1	AU145192	5.53
hypothetical protein R33729_1	AC005339	5.53
CDW52 antigen (CAMPATH-1 antigen)	NM_001803	5.52
ribosomal protein, large, P0	AI953822	5.51
actin related protein 2/3 complex, subunit 2 (34 kD)	AF279893	5.50
guanine nucleotide binding protein (G protein), beta polypeptide 2-	NM_006098	5.49

FIG. 4A-6

like 1

eukaryotic translation initiation factor 4A, isoform 1	BC006210	5.47
ubiquitin C	AB009010	5.47
polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	AW402635	5.40
hypothetical protein MGC4675	AL118502	5.39
ribosomal protein L10	NM_006013	5.35
v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	M79321	5.33
calpain, small subunit 1	AD001527	5.31
lymphocyte-specific protein tyrosine kinase	NM_005356	5.31
anaphase promoting complex subunit 5	BC001081	5.29
ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	BG395660	5.29
kinesin 2 (60-70kD)	AA284075	5.29
hematological and neurological expressed 1	NM_016185	5.27
ribosomal protein, large, P0	BC005863	5.26
immunoglobulin heavy constant mu	S74639	5.25
proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7)	U17496	5.24
ribosomal protein S3	U14990	5.22
proteasome (prosome, macropain) 26S subunit, ATPase, 3	AL545523	5.21
coronin, actin binding protein, 1A	U34690	5.19
nuclear distribution gene C (A.nidulans) homolog	AF241788	5.17
neutrophil cytosolic factor 4 (40kD)	NM_000631	5.17
gb:M24668.1 /DEF=Human Ig rearranged H-chain V-region mRNA (C-D-JH4), complete cds. /FEA=mRNA /GEN=IGH@ /DB_XREF=gi:185198 /FL=gb:M24668.1	M24668	5.16
splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	NM_006924	5.16
Cw1 antigen	M12679	5.11
ariadne homolog 2 (Drosophila)	BC000422	5.09
bromodomain-containing 2	D42040	5.09
major histocompatibility complex, class I, F	AW514210	5.08
succinate dehydrogenase complex, subunit B, iron sulfur (lp)	NM_003000	5.08
NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)	NM_004551	5.07
farnesyl-diphosphate farnesyltransferase 1	BC003573	5.01
transgelin 2	NM_003564	4.98
cytochrome c oxidase subunit IV isoform 1	NM_001861	4.98
integrin beta 4 binding protein	AF022229	4.95
HIF-1 responsive RTP801	NM_019058	4.93
hypothetical protein PRO1068	NM_018573	4.90
putative breast adenocarcinoma marker (32kD)	NM_014453	4.88
protein tyrosine phosphatase, receptor type, O	U20489	4.88
hypothetical protein DKFZp434N185	NM_025205	4.86
tubulin alpha 6	BC005946	4.85
ribosomal protein L13	AA789278	4.85
Lysosomal-associated multispanning membrane protein-5	AI589086	4.83
protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue	M18468	4.83

FIG. 4A-7

specific extinguisher 1)		
ribosomal protein, large P2	NM_001004	4.82
eukaryotic translation initiation factor 4 gamma, 1	AF104913	4.79
transcription elongation factor B (SIII), polypeptide 2 (18kD, elongin B)	NM_007108	4.78
karyopherin (importin) beta 3	NM_002271	4.76
lymphocyte cytosolic protein 1 (L-plastin)	J02923	4.74
peroxiredoxin 1	L19184	4.70
heat shock protein 75	NM_016292	4.70
HLA-G histocompatibility antigen, class I, G	AF226990	4.70
ribosomal protein S14	AF116710	4.69
cullin 1	NM_003592	4.69
heat shock 70kD protein 4	BC002526	4.66
NADH dehydrogenase (ubiquinone) flavoprotein 1 (51kD)	AF092131	4.65
HSPC274 protein	NM_014145	4.63
Consensus includes gb:BE305165 /FEA=EST /DB_XREF=gi:9177184 /DB_XREF=est:601186685T1 /CLONE=IMAGE:2959580 /UG=Hs.100623 phospholipase C, beta 3, neighbor pseudogene	BE305165	4.60
MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	D55716	4.60
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	NM_003406	4.56
lymphoid-restricted membrane protein	U10485	4.55
tumor protein D52	BG389015	4.53
small nuclear ribonucleoprotein polypeptides B and B1	J04564	4.53
postmeiotic segregation increased 2-like 9	U38979	4.52
v-myb myeloblastosis viral oncogene homolog (avian)-like 2	NM_002466	4.51
T cell receptor beta locus	AF043179	4.46
7-dehydrocholesterol reductase	AW150953	4.45
hypothetical protein FLJ20113	AL523776	4.45
eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD)	BC000733	4.44
baculoviral IAP repeat-containing 5 (survivin)	AB028869	4.41
lymphoid-restricted membrane protein	NM_006152	4.39
APEX nuclease (multifunctional DNA repair enzyme)	M80261	4.39
Consensus includes gb:Z82202 /DEF=Human DNA sequence from clone RP1-34P24 on chromosome 22 Contains a pseudogene similar to ribosomal protein L35, ESTs, STSs and GSSs /FEA=CDS /DB_XREF=gi:4107193 /UG=Hs.247778 Human DNA sequence from clone RP1-34P24 on c	Z82202	4.39
HSV1 binding protein	NM_018694	4.39
U6 snRNA-associated Sm-like protein	AA112507	4.38
T cell receptor beta locus	AL559122	4.38
casein kinase 2, beta polypeptide	NM_001320	4.38
putative methyltransferase	NM_017528	4.37
VPS28 protein	NM_016208	4.35
lysosomal-associated membrane protein 1	NM_005561	4.33
bone marrow stromal cell antigen 2	NM_004335	4.32

FIG. 4A-8

ribosomal protein L13a	BF942308	4.32
transmembrane protein 4	BC001027	4.32
calreticulin	AD000092	4.30
nuclear RNA export factor 1	BC004904	4.30
polymerase (RNA) II (DNA directed) polypeptide E (25kD)	AI554759	4.28
nucleosome assembly protein 1-like 4	NM_005969	4.25
gb:AY014272.1 /DEF=Homo sapiens FKSG30 (FKSG30) mRNA, complete cds. /FEA=mRNA /GEN=FKSG30 /PROD=FKSG30 /DB_XREF=gi:12408251 /UG=Hs.315492 Homo sapiens FKSG30 (FKSG30) mRNA, complete cds /FL=gb:AY014272.1	AY014272	4.25
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc-regulated)	NM_006773	4.24
KIAA0618 gene product	AI768378	4.23
LIM domain only 2 (rhombotin-like 1)	NM_005574	4.23
non-POU-domain-containing, octamer-binding	BC003129	4.22
peptidylprolyl isomerase F (cyclophilin F)	NM_005729	4.19
zinc finger protein 207	BE871379	4.19
emopamil binding protein (sterol isomerase)	AV702405	4.18
unknown	NM_016209	4.17
HS1 binding protein	NM_006118	4.17
aconitase 2, mitochondrial	NM_001098	4.16
H3 histone, family 3B (H3.3B)	NM_005324	4.15
C2f protein	U72514	4.14
ribosomal protein L13a	BC001675	4.14
replication protein A1 (70kD)	NM_002945	4.12
proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	NM_002808	4.12
interferon-related developmental regulator 1	NM_001550	4.11
HLA-G histocompatibility antigen, class I, G	M90684	4.11
RNB6	NM_016337	4.11
RNA binding motif protein 5	U23946	4.10
signal sequence receptor, beta (translocon-associated protein beta)	NM_003145	4.09
guanine nucleotide binding protein (G protein), beta polypeptide 2	NM_005273	4.09
ribosomal protein S26	NM_001029	4.08
T cell receptor alpha locus	M12423	4.07
translocase of inner mitochondrial membrane 13 homolog B (yeast)	NM_012458	4.07
flap structure-specific endonuclease 1	NM_004111	4.06
translocating chain-associating membrane protein	NM_014294	4.06
KIAA0217 protein	BC003381	4.06
translocase of inner mitochondrial membrane 10 homolog (yeast)	NM_012456	4.05
MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B)	NM_005919	4.04
tubulin alpha 6	BC004949	4.03
major histocompatibility complex, class I, E	M31183	4.03
fuse-binding protein-interacting repressor	AF217197	4.02
FK506 binding protein 1A (12kD)	BC005147	4.02

FIG. 4A-9

ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	AI587323	4.01
DNA replication factor	AF321125	4.00
HLA-B associated transcript 3	BG028844	4.00
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (14.5kD, B14.5a)	NM_005001	4.00
poly(rC) binding protein 1	U24223	4.00
tetraspan 3	NM_005724	3.99
hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	AI972144	3.99
cyclin-dependent kinase 4	NM_000075	3.98
solute carrier family 2 (facilitated glucose/fructose transporter), member 5	BE560461	3.98
hypothetical protein	BG257762	3.98
T cell receptor alpha locus	M15565	3.96
actin related protein 2/3 complex, subunit 1A (41 kD)	NM_006409	3.95
T cell receptor alpha locus	L34703	3.94
amyloid beta (A4) precursor-like protein 2	AW001847	3.94
translocase of inner mitochondrial membrane 23 homolog (yeast)	NM_006327	3.93
B-cell translocation gene 1, anti-proliferative	AL535380	3.93
PAI-1 mRNA-binding protein	BC003049	3.92
adenylate kinase 2	U39945	3.92

FIG. 4B-1

gene	NCBI Accession Number	FOLD DECREASE
Consensus includes gb:AA292281 /FEA=EST /DB_XREF=gi:1940261 /DB_XREF=est:zt51b03.s1 /CLONE=IMAGE:725837 /UG=Hs.181307 H3 histone, family 3A	AA292281	15.15
calreticulin	AI378706	13.38
ribosomal protein S11	BF680255	10.86
ribosomal protein S19	BC000023	9.95
ribosomal protein, large P2	BC005354	9.72
Consensus includes gb:AW302047 /FEA=EST /DB_XREF=gi:6711724 /DB_XREF=est:xr52f08.x1 /CLONE=IMAGE:2763783 /UG=Hs.76230 ribosomal protein S10	AW302047	8.60
Consensus includes gb:L48784 /DEF=050 Homo sapiens cDNA /FEA=mRNA /DB_XREF=gi:1066715 /UG=Hs.182426 ribosomal protein S2	L48784	7.68
Consensus includes gb:AJ249377.1 /DEF=Homo sapiens partial mRNA for human Ig lambda light chain variable region, clone MB91 (331 bp). /FEA=mRNA /GEN=IGLV /PROD=immunoglobulin lambda variable region /DB_XREF=gi:5911837 /UG=Hs.247898 Human anti-streptococ	AJ249377	7.66
Consensus includes gb:D84143.1 /DEF=Human immunoglobulin (mAb59) light chain V region mRNA, partial sequence. /FEA=mRNA /PROD=immunoglobulin light chain V-J region /DB_XREF=gi:1255613 /UG=Hs.121508 Human immunoglobulin (mAb59) light chain V region mRNA,	D84143	7.60
ribosomal protein L27a	BE737027	6.93
emopamil binding protein (sterol isomerase)	N58493	6.41
calreticulin	AA910371	5.40
hypothetical protein PRO1843	NM_018507	5.23
Cluster Incl. AI201594:qc02h12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1708487 /clone_end=3 /gb=AI201594 /gi=3754200 /ug=Hs.239333 /len=591	AI201594	4.91
ribosomal protein S20	AF113008	4.69
C-terminal binding protein 1	BF984434	4.57
KIAA0906 protein	AA909765	4.45
ribosomal protein L27	BE312027	4.42
Consensus includes gb:AF044592 /DEF=Homo sapiens lymphocyte-predominant Hodgkins disease case 4 immunoglobulin heavy chain gene, variable region, partial cds /FEA=CDS /DB_XREF=gi:2852420 /UG=Hs.248077 Homo sapiens lymphocyte-predominant Hodgkins disease	AF044592	4.24
hypothetical protein FLJ21034	NM_024940	4.13
aminopeptidase puromycin sensitive	BG153399	4.04
immunoglobulin lambda locus	AF043586	4.00
Consensus includes gb:AJ239383.1 /DEF=Homo sapiens mRNA	AJ239383	3.96

FIG. 4B-2

for immunoglobulin heavy chain variable region, ID 31. /FEA=mRNA /GEN=IGHV /PROD=immunoglobulin heavy chain variable region /DB_XREF=gi:4456587 /UG=Hs.249245 Homo sapiens mRNA for single-chain anti killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	X93596	3.81
hypothetical protein FLJ12619	BE465032	3.81
lymphoid blast crisis oncogene	AF127481	3.78
Consensus includes gb:AV719355 /FEA=EST /DB_XREF=gi:10816507 /DB_XREF=est:AV719355 /CLONE=GLCEMB06 /UG=Hs.97109 ESTs	AV719355	3.67
alanine-glyoxylate aminotransferase 2-like 1	NM_031279	3.63
Cluster Incl. AI949010:wq36a07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2473332 /clone_end=3 /gb=AI949010 /gi=5741320 /ug=Hs.104036 /len=457	AI949010	3.59
PCTAIRE protein kinase 1	NM_006201	3.56
ADP-ribosylation factor 6	AA243143	3.49
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	AA502643	3.42
Consensus includes gb:BF973387 /FEA=EST /DB_XREF=gi:12340602 /DB_XREF=est:602242353F1 /CLONE=IMAGE:4330861 /UG=Hs.305989 Human DNA sequence from clone RP3-483K16 on chromosome 6p12.1-21.1. Contains (parts of) two novel genes, RPS16 (40S Ribosomal protein	BF973387	3.42
G protein-coupled receptor kinase 6	BG423052	3.37
M10098 Human 18S rRNA sequence, length 1969 bases, middle target bases 647-1292	M10098	3.33
GM2 ganglioside activator protein	X61094	3.24
dystrophia myotonica-containing WD repeat motif	L19267	3.24
collagen, type I, alpha 1	AI743621	3.24
cathepsin S	BC002642	3.22
translation initiation factor IF2	AB018284	3.19
hypothetical protein FLJ22965	NM_022101	3.16
coactivator-associated arginine methyltransferase-1	AL529396	3.14
JTV1 gene	AF116615	3.13
RAB6 interacting, kinesin-like (rabkinesin 6)	NM_005733	3.10
hypothetical protein FLJ20666	NM_018333	3.06
isocitrate dehydrogenase 1 (NADP+), soluble	NM_005896	3.04
Consensus includes gb:AI524687 /FEA=EST /DB_XREF=gi:4438822 /DB_XREF=est:th12a07.x1 /CLONE=IMAGE:2118036 /UG=Hs.57969 phenylalanine-tRNA synthetase	AI524687	3.03
Consensus includes gb:AL136179 /DEF=Human DNA sequence from clone RP3-322L4 on chromosome 6. Contains the SOX4 gene for SRY (sex determining region Y)-box 4, a pseudogene similar to predicted fly, worm and yeast genes, ESTs, STSs, GSSs and four CpG islan	AL136179	3.03
nucleolar protein 4	NM_003787	3.02

FIG. 4B-3

ribosomal protein L38	AW303136	3.02
ribosomal protein L38	BC000603	2.98
Consensus includes gb:AW090043 /FEA=EST /DB_XREF=gi:6047387 /DB_XREF=est:xd01c05.x1 /CLONE=IMAGE:2592488 /UG=Hs.326464 Homo sapiens cDNA: FLJ21702 fis, clone COL09874	AW090043	2.91
Consensus includes gb:AW971415 /FEA=EST /DB_XREF=gi:8161260 /DB_XREF=est:EST383504 /UG=Hs.165337 ESTs	AW971415	2.90
J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	J04423	2.88
Consensus includes gb:AA890010 /FEA=EST /DB_XREF=gi:3016889 /DB_XREF=est:aj89h08.s1 /CLONE=IMAGE:1403679 /UG=Hs.50785 SEC22, vesicle trafficking protein (S. cerevisiae)-like 1	AA890010	2.88
gb:Z25437.1 /DEF=H.sapiens protein-tyrosine kinase gene, complete CDS. /FEA=mRNA /PROD=protein-tyrosine kinase /DB_XREF=gi:405752 /FL=gb:Z25437.1	Z25437	2.87
prefoldin 4	NM_002623	2.85
KIAA1046 protein	NM_014928	2.83
ATPase, H+ transporting, lysosomal (vacuolar proton pump) non- catalytic accessory protein 1A (110/116kD)	NM_005177	2.81
hypothetical protein FLJ10159	NM_018013	2.80
Consensus includes gb:BG109746 /FEA=EST /DB_XREF=gi:12603252 /DB_XREF=est:602280883F1 /CLONE=IMAGE:4368381 /UG=Hs.325625 Homo sapiens clone 23938 mRNA sequence	BG109746	2.79
HIV-1 rev binding protein 2	AI912583	2.76
acidic epididymal glycoprotein-like 1	X95238	2.75
hypothetical protein FLJ12619	AL136632	2.74
hypothetical protein FLJ14107	NM_025026	2.73
Escherichia coli /REF=J04423 /DEF=E coli bioB gene biotin synthetase corresponding to nucleotides 2393-2682 of J04423 /LEN=1114 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	J04423	2.73
E74-like factor 4 (ets domain transcription factor)	NM_001421	2.71
ribonuclease P, 40kD subunit	NM_006638	2.71
transducin (beta)-like 1	AA724134	2.70
cytochrome c oxidase subunit Vb	AI557312	2.70
RAB5B, member RAS oncogene family	AF267863	2.68
RAP2B, member of RAS oncogene family	NM_002886	2.67
ATP-binding cassette, sub-family D (ALD), member 3	NM_002858	2.67
Consensus includes gb:AK025724.1 /DEF=Homo sapiens cDNA: FLJ22071 fis, clone HEP11691. /FEA=mRNA /DB_XREF=gi:10438333 /UG=Hs.326248 Homo sapiens cDNA: FLJ22071 fis, clone HEP11691	AK025724	2.67
solute carrier family 21 (organic anion transporter), member 6	AB026257	2.65
Consensus includes gb:AW971134 /FEA=EST /DB_XREF=gi:8160979 /DB_XREF=est:EST383221 /UG=Hs.292245 ESTs, Weakly similar to ALU1_HUMAN ALU	AW971134	2.64

FIG. 4B-4

SUBFAMILY J SEQUENCE CONTAMINATION WARNING

ENTRY H.sapiens

orphan seven-transmembrane receptor, chemokine related	NM_016557	2.61
Consensus includes gb:AL050065.1 /DEF=Homo sapiens mRNA; cDNA DKFZp566M043 (from clone DKFZp566M043).		
/FEA=mRNA /DB_XREF=gi:4884295 /UG=Hs.212587 Homo sapiens mRNA; cDNA DKFZp566M043 (from clone DKFZp566M043)	AL050065	2.61
PAX transcription activation domain interacting protein 1 like	AI357401	2.60
cytoskeleton-associated protein 4	NM_006825	2.59
KIAA0653 protein, B7-like protein	AF289028	2.59
C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 6	AF200738	2.59
epithelial membrane protein 3	NM_001425	2.59
ribosomal protein L37a	BE857772	2.59
Consensus includes gb:AI345238 /FEA=EST /DB_XREF=gi:4082444 /DB_XREF=est:tb81b07.x1 /CLONE=IMAGE:2060725 /UG=Hs.111334 ferritin, light polypeptide	AI345238	2.59
ATPase, H+ transporting, lysosomal (vacuolar proton pump) 9kD	AI252582	2.58
Bloom syndrome	NM_000057	2.57
cytochrome P450 isoform 4F12	NM_023944	2.56
H3 histone family, member C	NM_003531	2.56
hypothetical protein FLJ22009	NM_024745	2.56
glycophorin E	NM_002102	2.55
hypothetical protein FLJ10298	NM_018050	2.55
endomucin-1	NM_016241	2.55
cyclin G2	AW134535	2.55
hexokinase 2	AI761561	2.54
polymerase (DNA directed), eta	NM_006502	2.53
cullin 5	NM_003478	2.53
PI-3-kinase-related kinase SMG-1	BE000837	2.52
PRO1880 protein	NM_014104	2.50
helicase KIAA0054	NM_014877	2.50
M10098 Human 18S rRNA gene, complete (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	M10098	2.50
KIAA0889 protein	NM_015377	2.49
hypothetical protein FLJ20897	AI335509	2.49
gamma-aminobutyric acid (GABA) A receptor, alpha 5	BF966183	2.49
translation initiation factor IF2	BE138647	2.48
SCAN domain-containing 2	AF244812	2.47
inhibin, beta C	NM_005538	2.47
M10098 Human 18S rRNA sequence, length 1969 bases, 3 prime target bases 1293-1938	M10098	2.47
cysteine-rich motor neuron 1	BG546884	2.47
mitochondrial ribosomal protein S12	R68573	2.47
hypothetical protein FLJ10357	NM_018071	2.47
mannan-binding lectin serine protease 1 (C4/C2 activating	BC000587	2.45

FIG. 4B-5

component of Ra-reactive factor)		
thiopurine S-methyltransferase	U12387	2.45
sorting nexin 4	AA524345	2.45
golgi associated, gamma adaptin ear containing, ARF binding protein 1	AW001443	2.45
Escherichia coli /REF=J04423 /DEF=E coli bioB gene biotin synthetase corresponding to nucleotides 2772-3004 of J04423 /LEN=1114 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	J04423	2.44
methionine adenosyltransferase II, alpha	AW301861	2.43
Consensus includes gb:AK022473.1 /DEF=Homo sapiens cDNA FLJ12411 fis, clone MAMMA1002964. /FEA=mRNA /DB_XREF=gi:10433882 /UG=Hs.296722 Homo sapiens cDNA FLJ12411 fis, clone MAMMA1002964	AK022473	2.43
eukaryotic translation initiation factor 5A	AA393940	2.42
tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcrption factor IIIA-interacting protein	NM_021980	2.42
J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	J04423	2.42
SH3-domain GRB2-like 3	AF036269	2.42
hypothetical protein FLJ13078	AK023140	2.41
serine/threonine-protein kinase PRP4 homolog	AA156948	2.41
harakiri, BCL2 interacting protein (contains only BH3 domain)	U76376	2.41
Consensus includes gb:AK021505.1 /DEF=Homo sapiens cDNA FLJ11443 fis, clone HEMBA1001330. /FEA=mRNA /DB_XREF=gi:10432701 /UG=Hs.297945 Homo sapiens cDNA FLJ11443 fis, clone HEMBA1001330	AK021505	2.40
glioma pathogenesis-related protein	U16307	2.40
artemis protein	AK022922	2.40
phosphodiesterase 10A	AF127480	2.40
ubiquitin specific protease 15	AF106069	2.38
TGFB-induced factor (TALE family homeobox)	NM_003244	2.38
PRO0478 protein	NM_014129	2.38
artemis protein	NM_022487	2.37
Consensus includes gb:AI915947 /FEA=EST /DB_XREF=gi:5635802 /DB_XREF=est:wg96e01.x1 /CLONE=IMAGE:2379096 /UG=Hs.28212 ESTs	AI915947	2.37
triple functional domain (PTPRF interacting)	AL161955	2.36
thromboxane A2 receptor	NM_001060	2.36
KIAA1655 protein	AB051442	2.36
Consensus includes gb:BF942161 /FEA=EST /DB_XREF=gi:12359481 /DB_XREF=est:nae87g10.x1 /CLONE=IMAGE:4118994 /UG=Hs.302797 ESTs	BF942161	2.35
DnaJ (Hsp40) homolog, subfamily A, member 1	AL534104	2.35
hypothetical protein FLJ22479	NM_024900	2.35
transforming, acidic coiled-coil containing protein 2	AF220152	2.35
KIAA0446 gene product	AB007915	2.34
DKFZP547E1010 protein	N92920	2.33

FIG. 4B-6

Consensus includes gb:AL157484.1 /DEF=Homo sapiens mRNA; cDNA DKFZp762M127 (from clone DKFZp762M127). /FEA=mRNA /DB_XREF=gi:7018527 /UG=Hs.22483 Homo sapiens mRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)	AL157484	2.33
kinectin 1 (kinesin receptor)	BF589024	2.33
colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	L29349	2.32
DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1	AI348378	2.32
hypothetical protein FLJ23548	NM_024590	2.32
MAD, mothers against decapentaplegic homolog (Drosophila) interacting protein, receptor activation anchor	NM_007323	2.32
Consensus includes gb:BC004344.1 /DEF=Homo sapiens, clone IMAGE:3633354, mRNA, partial cds. /FEA=mRNA /PROD=Unknown (protein for IMAGE:3633354) /DB_XREF=gi:13279286 /UG=Hs.5019 Homo sapiens, clone IMAGE:3633354, mRNA, partial cds	BC004344	2.32
Consensus includes gb:R33964 /FEA=EST /DB_XREF=gi:789822 /DB_XREF=est:yh74c03.r1 /CLONE=IMAGE:135460 /UG=Hs.288681 Homo sapiens cDNA FLJ11022 fis, clone PLACE1003771	R33964	2.31
prostate derived STE20-like kinase PSK	NM_016151	2.31
putative protein O-mannosyltransferase	NM_013382	2.30
Consensus includes gb:AK021440.1 /DEF=Homo sapiens cDNA FLJ11378 fis, clone HEMBA1000456. /FEA=mRNA /DB_XREF=gi:10432625 /UG=Hs.6937 hypothetical protein FLJ10276	AK021440	2.30
Consensus includes gb:AL080160.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434M054 (from clone DKFZp434M054). /FEA=mRNA /DB_XREF=gi:5262622 /UG=Hs.274517 Homo sapiens mRNA; cDNA DKFZp434M054 (from clone DKFZp434M054)	AL080160	2.30
uncharacterized hypothalamus protein HT011	BE565675	2.30
S-adenosylmethionine decarboxylase 1	NM_001634	2.29
Consensus includes gb:BE786164 /FEA=EST /DB_XREF=gi:10207362 /DB_XREF=est:601474273F1 /CLONE=IMAGE:3877146 /UG=Hs.80285 Homo sapiens mRNA; cDNA DKFZp586C1723 (from clone DKFZp586C1723)	BE786164	2.29
Consensus includes gb:BC005365.1 /DEF=Homo sapiens, clone IMAGE:3829438, mRNA, partial cds. /FEA=mRNA /PROD=Unknown (protein for IMAGE:3829438) /DB_XREF=gi:13529199 /UG=Hs.331237 Homo sapiens, clone IMAGE:3829438, mRNA, partial cds	BC005365	2.29
Consensus includes gb:AW971254 /FEA=EST /DB_XREF=gi:8161099 /DB_XREF=est:EST383343 /UG=Hs.178433 ESTs	AW971254	2.28
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	NM_006080	2.28
Consensus includes gb:AF164963.1 /DEF=Homo sapiens tumor antigen NA88-A pseudogene, complete sequence. /FEA=mRNA /DB_XREF=gi:5901726 /UG=Hs.306576 Homo sapiens tumor	AF164963	2.28

FIG. 4B-7

antigen NA88-A pseudogene, complete sequence		
immunoglobulin heavy constant mu	S55735	2.28
actin-related protein 3-beta	NM_020445	2.28
CDC14 cell division cycle 14 homolog A (S. cerevisiae)	NM_003672	2.27
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD)	NM_030881	2.27
PABP-interacting protein 2	AL043487	2.26
DnaJ (Hsp40) homolog, subfamily B, member 9	AL080081	2.26
alcohol dehydrogenase 1C (class I), gamma polypeptide	NM_000669	2.25
ecotropic viral integration site 2A	NM_014210	2.25
Consensus includes gb:A1126492 /FEA=EST		
/DB_XREF=gi:3595006 /DB_XREF=est:qd82h06.x1		
/CLONE=IMAGE:1736027 /UG=Hs.104258 Homo sapiens mRNA,		
exon 1, 2, 3, 4, clone:RES4-24A	A1126492	2.24
N-myristoyltransferase 2	NM_004808	2.24
J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent		
transcript regions 5 prime, Middle, and 3 prime respectively)	J04423	2.24
phosducin-like	NM_005388	2.24
hypothetical protein FLJ22558	NM_022747	2.24
peptidyl-prolyl isomerase G (cyclophilin G)	AW340788	2.23
KIAA0469 gene product	NM_014851	2.23
putative lymphocyte G0/G1 switch gene	NM_015714	2.23
Consensus includes gb:BE930512 /FEA=EST		
/DB_XREF=gi:10456588 /DB_XREF=est:RC6-GN0071-160800-		
021-D01 /UG=Hs.168732 ESTs	BE930512	2.23
A kinase (PRKA) anchor protein 1	BC000729	2.23
aldehyde dehydrogenase 4 family, member A1	U24267	2.23
Consensus includes gb:BF573849 /FEA=EST		
/DB_XREF=gi:11647561 /DB_XREF=est:602132053F1		
/CLONE=IMAGE:4271340 /UG=Hs.96343 ESTs, Weakly similar to		
ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!!		
H.sapiens	BF573849	2.22
ATPase, Class I, type 8B, member 1	BG252666	2.22
Consensus includes gb:A1701156 /FEA=EST		
/DB_XREF=gi:4989056 /DB_XREF=est:we10f09.x1		
/CLONE=IMAGE:2340713 /UG=Hs.6580 Homo sapiens cDNA:		
FLJ23227 fis, clone CAE00645, highly similar to AF052138 Homo		
sapiens clone 23718 mRNA sequence	A1701156	2.22
stress 70 protein chaperone, microsome-associated, 60kD	A1718418	2.22
gb:U61167.1 /DEF=Human SH3 domain-containing protein		
SH3P18 mRNA, complete cds. /FEA=mRNA /PROD=SH3 domain-		
containing protein SH3P18 /DB_XREF=gi:1438934		
/UG=Hs.330549 Human SH3 domain-containing protein SH3P18		
mRNA, complete cds /FL=gb:U61167.1	U61167	2.22
hypothetical protein FLJ23185	NM_025056	2.21
adenylate cyclase 7	NM_001114	2.21
Consensus includes gb:AL163202 /DEF=Homo sapiens		
chromosome 21 segment HS21C002 /FEA=CDS		
/DB_XREF=gi:7717242 /UG=Hs.289121 Homo sapiens		
chromosome 21 segment HS21C002	AL163202	2.21

FIG. 4B-8

helicase-moi	BF590131	2.21
Consensus includes gb:R06655 /FEA=EST /DB_XREF=gi:757275 /DB_XREF=est:yf10e02.r1 /CLONE=IMAGE:126458 /UG=Hs.188518 ESTs, Moderately similar to AF078844 1 hqp0376 protein H.sapiens	R06655	2.21
hypothetical protein FLJ23311	NM_024680	2.21
xylulokinase (H. influenzae) homolog	AA777793	2.21
islet cell autoantigen 1 (69kD)	BC005922	2.20
Escherichia coli /REF=J04423 /DEF=E coli bioB gene biotin synthetase corresponding to nucleotides 2071-2304 of J04423 /LEN=1114 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	J04423	2.20
degenerative spermatocyte homolog, lipid desaturase (Drosophila)	BC000961	2.20
high-mobility group 20B	BC002552	2.19
Consensus includes gb:AI984051 /FEA=EST /DB_XREF=gi:5811270 /DB_XREF=est:wt52h03.x1 /CLONE=IMAGE:2511125 /UG=Hs.11861 thyroid hormone receptor-associated protein, 240 kDa subunit /FL=gb:AF117754.1 gb:NM_005121.1	AI984051	2.19
Consensus includes gb:AI683552 /FEA=EST /DB_XREF=gi:4893734 /DB_XREF=est:tx67h02.x1 /CLONE=IMAGE:2274675 /UG=Hs.201605 ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens	AI683552	2.19
Consensus includes gb:AI393960 /FEA=EST /DB_XREF=gi:4223507 /DB_XREF=est:tg11d04.x1 /CLONE=IMAGE:2108455 /UG=Hs.274851 ESTs	AI393960	2.19
CGI-58 protein	NM_016006	2.19
PDZ domain containing guanine nucleotide exchange factor(GEF)1	AV654984	2.18
hypothetical protein FLJ12985	NM_024924	2.18
SHB adaptor protein (a Src homology 2 protein)	NM_003028	2.18
WNT1 inducible signaling pathway protein 3	AF143679	2.17
hypothetical protein FLJ20274	NM_017736	2.17
solute carrier family 16 (monocarboxylic acid transporters), member 7	NM_004731	2.17
Consensus includes gb:AA780524 /FEA=EST /DB_XREF=gi:2839855 /DB_XREF=est:ac71f01.s1 /CLONE=IMAGE:868057 /UG=Hs.294072 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens	AA780524	2.17
hypothetical protein FLJ12619	BG252842	2.17
M10098 Human 18S rRNA gene, complete (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	M10098	2.17
J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	J04423	2.17
coat protein gamma-cop	NM_016128	2.16
a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	NM_003183	2.16
ring finger protein 2	NM_007212	2.16

FIG. 4B-9

hypothetical protein FLJ10697	NM_018181	2.16
E3 ubiquitin ligase SMURF2	AY014180	2.16
kelch-like 2, Mayven (Drosophila)	NM_007246	2.16
Consensus includes gb:AK023911.1 /DEF=Homo sapiens cDNA FLJ13849 fis, clone THYRO1000865. /FEA=mRNA /DB_XREF=gi:10435992 /UG=Hs.181810 Homo sapiens cDNA FLJ13849 fis, clone THYRO1000865	AK023911	2.15
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)	AA993683	2.15
Cluster Incl. C18318:C18318 Homo sapiens cDNA, 5 end /clone=GEN-560E03 /clone_end=5 /gb=C18318 /gi=1579920 /ug=Hs.123469 /len=519	C18318	2.15
Consensus includes gb:AF043583.1 /DEF=Homo sapiens clone ASMneg1-b3 immunoglobulin lambda chain VJ region, (IGL) mRNA, partial cds. /FEA=mRNA /GEN=IGL /PROD=immunoglobulin lambda chain /DB_XREF=gi:2865477 /UG=Hs.248083 Homo sapiens clone ASMneg1-b3 immu	AF043583	2.15
hypothetical protein 384D8_6	BC000473	2.14
KIAA1659 protein	AB051446	2.13
Treacher Collins-Franceschetti syndrome 1	AW167713	2.13
Consensus includes gb:AA629050 /FEA=EST /DB_XREF=gi:2541437 /DB_XREF=est:zu84a06.s1 /CLONE=IMAGE:744658 /UG=Hs.50760 ESTs, Highly similar to BimL H.sapiens	AA629050	2.12
apolipoprotein L, 2	BC004395	2.12
type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	AF183569	2.12
Consensus includes gb:AL137378.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434K1126 (from clone DKFZp434K1126). /FEA=mRNA /DB_XREF=gi:6807908 /UG=Hs.306455 Homo sapiens mRNA; cDNA DKFZp434K1126 (from clone DKFZp434K1126)	AL137378	2.12
proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 synaptojanin 2	NM_002816	2.12
Consensus includes gb:AW970881 /FEA=EST /DB_XREF=gi:8160726 /DB_XREF=est:EST382964 /UG=Hs.205660 ESTs	AW970881	2.11
putative N6-DNA-methyltransferase	NM_013240	2.11
cathepsin D (lysosomal aspartyl protease)	A1560951	2.11
hematopoietic PBX-interacting protein	A1348545	2.11
tuftelin-interacting protein	NM_012143	2.11
phosphatidylinositol 4-kinase, catalytic, beta polypeptide	U81802	2.11
phosphoribosyl pyrophosphate synthetase 2	NM_002765	2.10
WW domain-containing protein 1	AU155187	2.10
Escherichia coli /REF=J04423 /DEF=E coli bioC protein corresponding to nucleotides 4257-4573 of J04423 /LEN=777 (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	J04423	2.09
carboxypeptidase N, polypeptide 2, 83kD	J05158	2.09
cofactor required for Sp1 transcriptional activation, subunit 9	BC005250	2.09

FIG. 4B-10

(33kD)		
carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	D12502	2.09
Consensus includes gb:AK026847.1 /DEF=Homo sapiens cDNA: FLJ23194 fis, clone REC00490. /FEA=mRNA		
/DB_XREF=gi:10439802 /UG=Hs.306887 Homo sapiens cDNA: FLJ23194 fis, clone REC00490	AK026847	2.09
NY-REN-58 antigen	NM_016122	2.09
solute carrier family 16 (monocarboxylic acid transporters), member 1	BF511091	2.08
transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	M74447	2.08
KIAA0669 gene product	NM_014779	2.08
GABA(A) receptors associated protein like 3	AF180519	2.08
cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19	X65962	2.08
choline/ethanolaminephosphotransferase	NM_006090	2.07
KIAA0304 gene product	AF105279	2.07
enolase 1, (alpha)	U88968	2.07
H2A histone family, member X	H51429	2.07
ALEX3 protein	NM_016607	2.07
Consensus includes gb:AK026825.1 /DEF=Homo sapiens cDNA: FLJ23172 fis, clone LNG10005. /FEA=mRNA		
/DB_XREF=gi:10439771 /UG=Hs.306885 Homo sapiens cDNA: FLJ23172 fis, clone LNG10005	AK026825	2.07
hypothetical protein FLJ20059	NM_017644	2.07
potassium inwardly-rectifying channel, subfamily J, member 8	NM_004982	2.07
early lymphoid activation protein	L22650	2.07
KIAA0874 protein	X80821	2.06
somatostatin receptor 4	NM_001052	2.06
tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	NM_025235	2.06
immunoglobulin heavy constant gamma 3 (G3m marker)	BF002659	2.06
transmembrane activator and CAML interactor	NM_012452	2.05
RAD54, S. cerevisiae, homolog of, B	NM_012415	2.05
polymerase (RNA) II (DNA directed) polypeptide B (140kD)	AW770896	2.05
FK506 binding protein 8 (38kD)	N95418	2.05
translation initiation factor IF2	BG261322	2.05
Consensus includes gb:AL050154.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586L0120 (from clone DKFZp586L0120). /FEA=mRNA /DB_XREF=gi:4884366 /UG=Hs.98314 Homo sapiens mRNA; cDNA DKFZp586L0120 (from clone DKFZp586L0120)	AL050154	2.05
Consensus includes gb:AU147017 /FEA=EST		
/DB_XREF=gi:11008538 /DB_XREF=est:AU147017		
/CLONE=HEMBB1002152 /UG=Hs.301905 Homo sapiens cDNA FLJ14080 fis, clone HEMBB1002152	AU147017	2.05
G protein-coupled receptor 1	AL046992	2.05
protease, serine, 21 (testisin)	NM_006799	2.05
hypothetical protein FLJ10496	NM_018114	2.05

FIG. 4B-11

pregnancy specific beta-1-glycoprotein 11	NM_002785	2.05
RAN binding protein 1	AI221318	2.04
hypothetical protein FLJ12151	AK022213	2.04
Consensus includes gb:AK022174.1 /DEF=Homo sapiens cDNA FLJ12112 fis, clone MAMMA1000043. /FEA=mRNA /DB_XREF=gi:10433510 /UG=Hs.288793 Homo sapiens cDNA FLJ12112 fis, clone MAMMA1000043	AK022174	2.04
transcription factor 4	AK026674	2.04
SRY (sex determining region Y)-box 4	AI989477	2.04
Consensus includes gb:AC004460 /DEF=Homo sapiens PAC clone RP5-1086D14 /FEA=CDS /DB_XREF=gi:2981263 /UG=Hs.307352 Homo sapiens PAC clone RP5-1086D14	AC004460	2.03
Consensus includes gb:AK023918.1 /DEF=Homo sapiens cDNA FLJ13856 fis, clone THYRO1000988. /FEA=mRNA /DB_XREF=gi:10436003 /UG=Hs.288489 Homo sapiens cDNA FLJ13856 fis, clone THYRO1000988	AK023918	2.03
SEC24 related gene family, member D (S. cerevisiae)	NM_014822	2.03
hypothetical protein FLJ11336	NM_018393	2.03
checkpoint suppressor 1	AA860806	2.03
Consensus includes gb:AF070647.1 /DEF=Homo sapiens clone 24438 mRNA sequence. /FEA=mRNA /DB_XREF=gi:3283921 /UG=Hs.124126 Homo sapiens clone 24438 mRNA sequence	AF070647	2.03
translin	AI659180	2.02
neuropilin 2	AA295257	2.02
cysteine-rich motor neuron 1	NM_016441	2.02
S100 calcium binding protein A11 (calgizzarin)	NM_005620	2.02
gb:NM_017648.1 /DEF=Homo sapiens hypothetical protein FLJ20063 (FLJ20063), mRNA. /FEA=mRNA /GEN=FLJ20063 /PROD=hypothetical protein FLJ20063 /DB_XREF=gi:8923068 /UG=Hs.5940 hypothetical protein FLJ20063 /FL=gb:AB035807.1 gb:NM_017648.1	NM_017648	2.02
PC4 and SFRS1 interacting protein 1	AF098482	2.02
immunoglobulin heavy constant mu	S74639	2.02
Consensus includes gb:AW301806 /FEA=EST /DB_XREF=gi:6711483 /DB_XREF=est:xr56e11.x1 /CLONE=IMAGE:2764172 /UG=Hs.150551 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens	AW301806	2.02
ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome)	BF588511	2.01
adducin 2 (beta)	NM_017482	2.01
thyroid hormone receptor-associated protein, 95-kD subunit	BG339606	2.01
hypothetical protein PRO1942	NM_018610	2.01
HCF-binding transcription factor Zhangfei	AI206560	2.01
protein phosphatase 2, regulatory subunit B (B56), gamma isoform	AW772123	2.01
cofactor required for Sp1 transcriptional activation, subunit 2 (150kD)	AK023368	2.00
F-box only protein 21	AK001699	2.00
gb:AF090895.1 /DEF=Homo sapiens clone HQ0117 PRO0117	AF090895	2.00

FIG. 4B-12

mRNA, complete cds. /FEA=mRNA /PROD=PRO0117		
/DB_XREF=gi:6690166 /UG=Hs.283919 Homo sapiens clone		
HQ0117 PRO0117 mRNA, complete cds /FL=gb:AF090895.1		
hypothetical protein PRO2849	NM_022335	2.00
Epstein-Barr virus induced gene 3	NM_005755	2.00
ATPase, Ca++ transporting, plasma membrane 1	L14561	2.00
tripartite motif-containing 2	NM_015271	2.00
brain-specific angiogenesis inhibitor 3	AB011122	2.00
Consensus includes gb:X78262.1 /DEF=H.sapiens mRNA for		
TRE5. /FEA=mRNA /DB_XREF=gi:587440 /UG=Hs.302178		
H.sapiens mRNA for TRE5		
	X78262	2.00
neuregulin 2	NM_013984	2.00
v-myc myelocytomatosis viral oncogene homolog 2 (avian)	NM_005377	1.99
calpain 9 (nCL-4)	AB038463	1.99
zinc finger protein 281	NM_012482	1.99
hypothetical protein LOC57187	BG403671	1.99
hypothetical protein FLJ13166	NM_025003	1.99
gastric inhibitory polypeptide receptor	NM_000164	1.99
activation-induced cytidine deaminase	NM_020661	1.99
caspase 8, apoptosis-related cysteine protease	BF439983	1.99
hypothetical protein FLJ20837	NM_017964	1.99
dickkopf homolog 2 (Xenopus laevis)	NM_014421	1.99
lipopolysaccharide specific response-68 protein	NM_018678	1.98
protein phosphatase, EF hand calcium-binding domain 2	NM_006239	1.98
hypothetical protein FLJ14346	NM_025029	1.98
membrane-spanning 4-domains, subfamily A, member 2 (Fc		
fragment of IgE, high affinity I, receptor for; beta polypeptide)		
Escherichia coli /REF=J04423 /DEF=E coli bioC protein		
corresponding to nucleotides 4609-4883 of J04423 /LEN=777 (-5		
and -3 represent transcript regions 5 prime and 3 prime		
respectively)		
	J04423	1.98
Consensus includes gb:BF035279 /FEA=EST		
/DB_XREF=gi:10743006 /DB_XREF=est:601457165F1		
/CLONE=IMAGE:3860633 /UG=Hs.20325 ESTs, Moderately		
similar to pot. ORF V H.sapiens		
	BF035279	1.98
KIAA1102 protein	AK027231	1.98
mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-		
acetylglucosaminyltransferase	NM_002408	1.98
ornithine decarboxylase antizyme inhibitor	AA047234	1.98
BLu protein	NM_015896	1.98
phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	NM_005028	1.98
clone FLB3816	NM_016415	1.98
thyroid hormone receptor interactor 11	BC002656	1.97
small inducible cytokine subfamily A (Cys-Cys), member 18,		
pulmonary and activation-regulated	Y13710	1.97
hypothetical protein FLJ13162	NM_025002	1.97
Homer, neuronal immediate early gene, 1B	BE550452	1.97
hypothetical protein FLJ14310	NM_025028	1.97

FIG. 4B-13

Consensus includes gb:U43604.1 /DEF=Human unidentified mRNA, partial sequence. /FEA=mRNA /DB_XREF=gi:1171236 /UG=Hs.159901 Human unidentified mRNA, partial sequence	U43604	1.97
hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	NM_000198	1.97
lipin 2	U55968	1.97
Consensus includes gb:AL050122.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586E121 (from clone DKFZp586E121). /FEA=mRNA /DB_XREF=gi:4884330 /UG=Hs.274511 Homo sapiens mRNA; cDNA DKFZp586E121 (from clone DKFZp586E121)	AL050122	1.97
gb:U96291.1 /DEF=Homo sapiens Ig kappa light chain variable region (VklI-A23) mRNA, complete cds. /FEA=mRNA /GEN=VklI-A23 /PROD=Ig kappa light chain variable region	U96291	1.97
/DB_XREF=gi:2345027 /UG=Hs.113273 Homo sapiens Ig kappa light chain variable region (Vkl	NM_022164	1.97
P3ECSL	AL044175	1.97
patched homolog (Drosophila)	AI734228	1.97
VW domain binding protein 4 (formin binding protein 21)	NM_004540	1.97
neural cell adhesion molecule 2	NM_018041	1.97
hypothetical protein FLJ10254	AA910614	1.96
ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	NM_021093	1.96
peptide YY, 2 (seminalplasmin)	AF116696	1.96
DnaJ (Hsp40) homolog, subfamily C, member 8	AK025933	1.96
KIAA0692 protein	AI769637	1.96
UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter	NM_017659	1.96
hypothetical protein FLJ20084	BF968960	1.96
beta-amyloid binding protein precursor	AL133646	1.96
glucocorticoid modulatory element binding protein 2	NM_000130	1.96
coagulation factor V (proaccelerin, labile factor)	N52532	1.96
KIAA0256 gene product	AK000864	1.96
Consensus includes gb:AK000864.1 /DEF=Homo sapiens cDNA FLJ10002 fis, clone HEMBA1000046. /FEA=mRNA	NM_022915	1.96
/DB_XREF=gi:7021188 /UG=Hs.296522 Homo sapiens cDNA FLJ10002 fis, clone HEMBA1000046		
mitochondrial ribosomal protein L44	AK022219	1.95
Consensus includes gb:AK022219.1 /DEF=Homo sapiens cDNA FLJ12157 fis, clone MAMMA1000500. /FEA=mRNA	BG029530	1.95
/DB_XREF=gi:10433569 /UG=Hs.98812 Homo sapiens cDNA FLJ12157 fis, clone MAMMA1000500	NM_018953	1.95
jumonji homolog (mouse)	U52696	1.95
homeo box C5	NM_014274	1.95
cAMP responsive element binding protein-like 1	NM_014809	1.95
Alu-binding protein with zinc finger domain	NM_002078	1.95
KIAA0319 gene product	BC001265	1.95
golgi autoantigen, golgin subfamily a, 4	NM_004696	1.94
hypothetical protein dJ462O23.2	AF220028	1.94
solute carrier family 16 (monocarboxylic acid transporters), member 4		
tripartite motif-containing 5		

FIG. 4B-14

integral membrane protein 2B	NM_021999	1.94
ATPase, Cu ⁺⁺ transporting, alpha polypeptide (Menkes syndrome)	NM_000052	1.94
cyclin E2	NM_004702	1.94
EphB3	X75208	1.94
hypothetical protein FLJ20097	NM_017667	1.94
DnaJ (Hsp40) homolog, subfamily B, member 9	NM_012328	1.94
polymerase (RNA) III (DNA directed) (32kD)	NM_006467	1.94
aldehyde dehydrogenase 1 family, member B1	BC001619	1.94
Consensus includes gb:AA017721 /FEA=EST		
/DB_XREF=gi:1479910 /DB_XREF=est:ze39f11.s1		
/CLONE=IMAGE:361389 /UG=Hs.49117 Homo sapiens mRNA;		
cDNA DKFZp564N1662 (from clone DKFZp564N1662)	AA017721	1.94
nuclear transcription factor Y, alpha	AL031778	1.94

FIG. 4C-1

Gene	NCBI Accession Number	FOLD INCREASE
gb:L23516.1 /DEF=Human Ig rearranged gamma-chain, V-DXP4-JH6c, complete cds. /FEA=mRNA /DB_XREF=gi:385218 /FL=gb:L23516.1	L23516	43.37
ubiquitin carrier protein	NM_014501	41.83
glyceraldehyde-3-phosphate dehydrogenase	M33197	41.07
Lysosomal-associated multispinning membrane protein-5	NM_006762	37.81
ribosomal protein L29	NM_000992	37.44
gb:L23518.1 /DEF=Human Ig rearranged gamma-chain, V-DXP1-JH4b, complete cds. /FEA=mRNA /DB_XREF=gi:385220 /FL=gb:L23518.1	L23518	37.23
immunoglobulin heavy constant mu	U80139	33.58
adaptor-related protein complex 2, mu 1 subunit	NM_004068	32.97
heat shock 90kD protein 1, beta	A1218219	32.61
macrophage migration inhibitory factor (glycosylation-inhibiting factor)	NM_002415	30.90
ferritin, light polypeptide	BG538564	30.50
ornithine decarboxylase antizyme 1	AF090094	30.15
Consensus includes gb:L48784 /DEF=050 Homo sapiens cDNA /FEA=mRNA /DB_XREF=gi:1066715 /UG=Hs.182426 ribosomal protein S2	L48784	30.09
enolase 1, (alpha)	U88968	28.76
ribosomal protein L29	BF683426	28.60
ribosomal protein L18	NM_000979	28.20
ribosomal protein L18a	NM_000980	28.19
chaperonin containing TCP1, subunit 7 (eta)	NM_006429	27.91
immunoglobulin heavy constant mu	BG340548	27.05
HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae)	NM_001536	25.89
profilin 1	NM_005022	24.23
procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	NM_000918	23.95
procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	J02783	23.56
Consensus includes gb:D84143.1 /DEF=Human immunoglobulin (mAb59) light chain V region mRNA, partial sequence. /FEA=mRNA /PROD=immunoglobulin light chain V-J region /DB_XREF=gi:1255613 /UG=Hs.121508 Human immunoglobulin (mAb59) light chain V region mRNA,	D84143	22.30
Consensus includes gb:AJ249377.1 /DEF=Homo sapiens partial mRNA for human Ig lambda light chain variable region, clone MB91 (331 bp). /FEA=mRNA /GEN=IGLV	AJ249377	21.91

FIG. 4C-2

/PROD=immunoglobulin lambda variable region		
/DB_XREF=gi:5911837 /UG=Hs.247898 Human anti-streptococ		
U6 snRNA-associated Sm-like protein LSm7	NM_016199	21.63
polymerase (DNA directed), delta 2, regulatory subunit (50kD)	NM_006230	21.62
ribosomal protein L8	NM_000973	21.19
transketolase (Wernicke-Korsakoff syndrome)	BF696840	21.11
gb:AJ225092.1 /DEF=Homo sapiens mRNA for single-chain antibody, complete cds. /FEA=CDS /PROD=immunoglobulin		
/DB_XREF=gi:3090425 /UG=Hs.249245 Homo sapiens mRNA for single-chain antibody, complete cds /FL=gb:AJ225092.1		
eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)	AJ225092	20.48
T-cell leukemia/lymphoma 1A	BC001173	19.28
ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	X82240	19.19
eukaryotic translation initiation factor 3, subunit 8 (110kD)	AA910614	19.08
gb:L07950.1 /DEF=Homo sapiens MHC class I HLA B71 mRNA, complete cds. /FEA=CDS /GEN=HLA-B /PROD=MHC HLA B71	BC000533	18.47
/DB_XREF=gi:307236 /FL=gb:L07950.1		
glyceraldehyde-3-phosphate dehydrogenase	L07950	17.83
MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	M33197	17.71
eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)	AF279900	17.26
pyruvate kinase, muscle	NM_003751	16.97
replication factor C (activator 1) 2 (40kD)	NM_002654	16.81
glyceraldehyde-3-phosphate dehydrogenase	M87338	16.75
spermidine synthase	BF689355	16.61
RNA polymerase II transcriptional regulation mediator (Med6, S. cerevisiae, homolog of)	NM_003132	16.57
Rab acceptor 1 (prenylated)	NM_005466	16.27
ribosomal protein L13	NM_006423	16.24
Consensus includes gb:D84140.1 /DEF=Human immunoglobulin (mAb56) light chain V region mRNA, partial sequence.	AW574664	16.05
/FEA=mRNA /PROD=immunoglobulin light chain V-J region		
/DB_XREF=gi:1255610 /UG=Hs.248043 Human immunoglobulin (mAb56) light chain V region mRNA,		
CD22 antigen	D84140	15.99
neutrophil cytosolic factor 4 (40kD)	X52785	15.89
small EDRK-rich factor 2	NM_013416	15.70
glyceraldehyde-3-phosphate dehydrogenase	NM_005770	15.52
transketolase (Wernicke-Korsakoff syndrome)	BE561479	15.36
ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit	L12711	15.06
CGI-135 protein	BE798517	14.96
glucose phosphate isomerase	NM_016068	14.94
pinin, desmosome associated protein	NM_000175	14.88
actin, beta	AF112222	14.86
Consensus includes gb:AF254822 /DEF=Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced /FEA=CDS_2 /DB_XREF=gi:10946127 /UG=Hs.78202	X00351	14.30
SWISNF related, matrix associated, actin dependent regulator of	AF254822	14.20

FIG. 4C-3

chromatin, subfamily a, memb		
fusion, derived from t(12;16) malignant liposarcoma	NM_004960	14.10
ribosomal protein S5	NM_001009	13.79
polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	BG335629	13.39
heat shock 90kD protein 1, beta	AF275719	13.32
nuclease sensitive element binding protein 1	BE966374	13.25
ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit	NM_001687	13.24
eukaryotic translation initiation factor 3, subunit 8 (110kD)	AA679705	13.07
immunoglobulin heavy constant mu	BC001872	13.03
actin, beta	X00351	12.99
serine hydroxymethyltransferase 2 (mitochondrial)	NM_005412	12.93
polymerase (RNA) II (DNA directed) polypeptide E (25kD)	AI554759	12.83
maternal G10 transcript	NM_003910	12.80
major histocompatibility complex, class I, B	D83043	12.59
cell death-regulatory protein GRIM19	NM_015965	12.48
proteasome (prosome, macropain) 26S subunit, ATPase, 3	AL545523	12.22
valosin-containing protein	AF100752	12.15
nuclear RNA helicase, DECD variant of DEAD box family	NM_005804	11.98
eukaryotic translation initiation factor 3, subunit 8 (110kD)	NM_003752	11.83
coronin, actin binding protein, 1A	U34690	11.81
mitochondrial ribosomal protein S12	NM_021107	11.76
cold inducible RNA binding protein	NM_001280	11.67
DEAD-box protein abstrakt	NM_016222	11.65
putative transmembrane protein; homolog of yeast Golgi		
membrane protein Yif1p (Yip1p-interacting factor)	NM_020470	11.52
protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	NM_002707	11.46
immunoglobulin heavy constant mu	S74639	11.35
acid phosphatase 1, soluble	BG035989	11.32
CGI-51 protein	NM_015380	11.29
ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	AL080089	11.11
7-dehydrocholesterol reductase	AW150953	11.06
B lymphoid tyrosine kinase	NM_001715	11.05
chaperonin containing TCP1, subunit 3 (gamma)	NM_005998	10.96
cell division cycle 2-like 2	AF067524	10.85
dolichyl-diphosphooligosaccharide-protein glycosyltransferase	D29643	10.84
transforming growth factor, beta 1	BC000125	10.80
ubiquinol-cytochrome c reductase core protein I	NM_003365	10.71
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3 (9kD, B9)	NM_004542	10.61
mitochondrial ribosomal protein S2	NM_016034	10.58
chaperonin containing TCP1, subunit 2 (beta)	AL545982	10.54
ribosomal protein L18a	AC004692	10.40
polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	AW402635	10.24
interferon stimulated gene (20kD)	NM_002201	10.17

FIG. 4C-4

gb:M24668.1 /DEF=Human Ig rearranged H-chain V-region mRNA (C-D-JH4), complete cds. /FEA=mRNA /GEN=IGH@		
/DB_XREF=gi:185198 /FL=gb:M24668.1	M24668	10.01
proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	NM_002812	9.92
proteasome (prosome, macropain) subunit, alpha type, 7	AL078633	9.84
ribosomal protein S19	BE259729	9.82
major histocompatibility complex, class II, DR beta 5	AJ297586	9.71
kinesin 2 (60-70kD)	AA284075	9.67
similar to HYPOTHETICAL 34.0 KDA PROTEIN ZK795.3 IN CHROMOSOME IV	BE747342	9.65
phosphoserine aminotransferase	NM_021154	9.50
solute carrier family 2 (facilitated glucose/fructose transporter), member 5	BE560461	9.50
mutS homolog 6 (E. coli)	D89646	9.48
gb:U62824.1 /DEF=Homo sapiens HLA class I heavy chain (HLA-Cw*1701) mRNA, complete cds. /FEA=CDS /GEN=HLA-Cw*1701		
/PROD=HLA class I heavy chain /DB_XREF=gi:1575443		
/UG=Hs.287811 H.sapiens mRNA for HLA-C alpha chain (Cw*1701) /FL=gb:U62824.1	U62824	9.44
major histocompatibility complex, class I, B	L42024	9.43
stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	BE886580	9.39
nucleosome assembly protein 1-like 4	NM_005969	9.31
proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	AB033605	9.29
ribosomal protein S19	NM_001022	9.29
replication factor C (activator 1) 2 (40kD)	NM_002914	9.28
eukaryotic translation initiation factor 4 gamma, 1	AF104913	9.27
glutathione S-transferase pi	NM_000852	9.15
signal sequence receptor, delta (translocon-associated protein delta)	NM_006280	9.05
VPS28 protein	NM_016208	9.01
DKFZP564M182 protein	AK000822	8.99
6-phosphogluconolactonase	NM_012088	8.94
ribosomal protein S2	NM_002952	8.88
protein phosphatase 1, regulatory subunit 7	BF718769	8.85
ribosomal protein S15	NM_001018	8.78
translocase of inner mitochondrial membrane 13 homolog B (yeast)	NM_012458	8.77
endothelial differentiation-related factor 1	AB002282	8.75
T cell receptor beta locus	M15564	8.72
hypothetical protein R33729_1	AC005339	8.61
ubiquitin C	M26880	8.53
major histocompatibility complex, class II, DR alpha	M60333	8.52
non-POU-domain-containing, octamer-binding	L14599	8.52
major histocompatibility complex, class II, DR alpha	M60334	8.36
DNA replication factor	AF321125	8.34
PRP8 pre-mRNA processing factor 8 homolog (yeast)	NM_006445	8.28
SKB1 homolog (S. pombe)	NM_006109	8.28

FIG. 4C-5

eukaryotic translation elongation factor 1 alpha 1	AL035687	8.27
KIAA0217 protein	BC003381	8.24
major histocompatibility complex, class II, DR beta 1	U65585	8.20
ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing)	NM_003334	8.14
polymerase (RNA) III (DNA directed) polypeptide K (12.3 kDa)	NM_016310	8.11
ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit f, isoform 2	NM_004889	8.06
glutaminyl-tRNA synthetase	NM_005051	8.04
HLA-B associated transcript 1	NM_004640	8.01
Consensus includes gb:AF043584.1 /DEF=Homo sapiens clone ASMneg1-b1 immunoglobulin lambda chain VJ region, (IGL) mRNA, partial cds. /FEA=mRNA /GEN=IGL /PROD=immunoglobulin lambda chain /DB_XREF=gi:2865479 /UG=Hs.287815 Homo sapiens clone ASMneg1-b1 immu	AF043584	8.00
ribosomal protein S14	AF116710	7.98
interferon regulatory factor 4	NM_002460	7.94
T cell receptor beta locus	AF043179	7.91
HLA-B associated transcript 3	BG028844	7.90
bone marrow stromal cell antigen 2	NM_004335	7.84
integrin beta 4 binding protein	AF022229	7.76
putative breast adenocarcinoma marker (32kD)	NM_014453	7.65
polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)	BC005903	7.63
hypothetical protein PRO1847	AF119855	7.60
D123 gene product	NM_006023	7.54
actin binding LIM protein 1	NM_006720	7.53
eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)	U36764	7.47
T cell receptor beta locus	AL559122	7.45
tubulin, beta, 4	AL565749	7.39
coatamer protein complex, subunit epsilon	NM_007263	7.35
chromosome 14 open reading frame 3	NM_012111	7.35
major histocompatibility complex, class II, DP alpha 1	M27487	7.30
mitochondrial ribosomal protein S34	NM_023936	7.28
hepatitis delta antigen-interacting protein A	NM_006848	7.27
peptidylprolyl isomerase F (cyclophilin F)	NM_005729	7.26
nuclear RNA export factor 1	BC004904	7.24
ubiquitin C	AB009010	7.21
transmembrane protein 4	BC001027	7.20
amyloid beta (A4) precursor-like protein 2	AW001847	7.19
hypothetical protein FLJ20113	AL523776	7.19
GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	AI697055	7.16
NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	AF155235	7.15
eukaryotic translation initiation factor 4A, isoform 1	NM_001416	7.13
macrophage erythroblast attacher	NM_005882	7.11
chemokine (C-X-C motif), receptor 4 (fusin)	AF348491	7.10
calreticulin	AD000092	7.09
ancient ubiquitous protein 1	NM_012103	7.07

FIG. 4C-6

emopamil binding protein (sterol isomerase)	AV702405	7.06
putative human HLA class II associated protein I	BE560202	7.05
suppression of tumorigenicity 14 (colon carcinoma, matriptase, epithin)	NM_021978	7.05
proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	NM_002809	7.02
GDP-mannose 4,6-dehydratase	NM_001500	7.01
transcription factor Dp-1	NM_007111	7.01
v-myb myeloblastosis viral oncogene homolog (avian)-like 2	NM_002466	6.90
origin recognition complex, subunit 5-like (yeast)	AF081459	6.89
Consensus includes gb:AF005487.1 /DEF=Homo sapiens MHC class II antigen (DRB6) mRNA, HLA-DRB6*0201 allele, sequence. /FEA=mRNA /DB_XREF=gi:5915893 /UG=Hs.167385 Homo sapiens MHC class II antigen HLA-DRB6 mRNA, partial cds	AF005487	6.89
splicing factor, arginine/serine-rich 5	AW084582	6.88
Consensus includes gb:BE305165 /FEA=EST /DB_XREF=gi:9177184 /DB_XREF=est:601186685T1 /CLONE=IMAGE:2959580 /UG=Hs.100623 phospholipase C, beta 3, neighbor pseudogene	BE305165	6.88
ATP-binding cassette, sub-family F (GCN20), member 2	NM_005692	6.87
adaptor-related protein complex 2, sigma 1 subunit	NM_021575	6.86
U6 snRNA-associated Sm-like protein	NM_012321	6.86
unknown	NM_016209	6.85
major histocompatibility complex, class I, F	AW514210	6.84
ribosomal protein S2	A1183766	6.82
HSV1 binding protein	NM_018694	6.81
CD79A antigen (immunoglobulin-associated alpha)	NM_001783	6.81
major histocompatibility complex, class II, DR beta 4	NM_021983	6.80
FK506 binding protein precursor	NM_016594	6.77
eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD)	BC000733	6.77
ADP-ribosylation factor 1	AA580004	6.76
hypothetical protein	NM_016459	6.74
anaphase promoting complex subunit 5	BC001081	6.74
U6 snRNA-associated Sm-like protein	AA112507	6.69
eukaryotic translation elongation factor 2	NM_001961	6.68
hypothetical protein MGC4675	AL118502	6.67
guanylate kinase 1	BC006249	6.66
SNRPN upstream reading frame	NM_022804	6.64
mitochondrial ribosomal protein L23	A1832239	6.62
RNA, U2 small nuclear	BC003629	6.58
membrane-spanning 4-domains, subfamily A, member 1	X12530	6.57
heat shock protein 75	NM_016292	6.51
transgelin 2	NM_003564	6.50
tryptophanyl-tRNA synthetase	M61715	6.47
actin, gamma 1	AL567820	6.46
eukaryotic translation initiation factor 4A, isoform 1	BC006210	6.45
guanine nucleotide binding protein (G protein), beta polypeptide 1	A1741124	6.45
ribosomal protein, large, P0	A1953822	6.43

FIG. 4C-7

ribonucleotide reductase M1 polypeptide	AI692974	6.42
proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	NM_002808	6.42
CD27-binding (Siva) protein	NM_006427	6.38
small nuclear ribonucleoprotein polypeptides B and B1	J04564	6.36
membrane-spanning 4-domains, subfamily A, member 1	BC002807	6.33
ribosomal protein, large, P0	NM_001002	6.32
ribosomal protein, large, P0	BC005863	6.30
seb4D	AL109955	6.28
ribosomal protein, large, P0	BC003655	6.28
mitochondrial ribosomal protein S16	NM_016065	6.26
CD27-binding (Siva) protein	AF033111	6.23
sterol regulatory element binding transcription factor 2	NM_004599	6.23
CDW52 antigen (CAMPATH-1 antigen)	NM_001803	6.21
ribosomal protein L10	NM_006013	6.21
cytochrome c oxidase subunit IV isoform 1	NM_001861	6.19
ribosomal protein S3	U14990	6.17
hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	AI972144	6.15
neutrophil cytosolic factor 4 (40kD)	NM_000631	6.15
NADH dehydrogenase (ubiquinone) flavoprotein 1 (51kD)	AF092131	6.14
aconitase 2, mitochondrial	NM_001098	6.11
ribosomal protein S26	NM_001029	6.11
HLA-G histocompatibility antigen, class I, G	AF226990	6.10
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	AI744900	6.08
DNA segment on chromosome 19 (unique) 1177 expressed sequence	NM_006114	6.08
ribosomal protein L13	AA789278	6.05
proteasome (prosome, macropain) subunit, beta type, 7	NM_002799	6.05
lymphocyte-specific protein tyrosine kinase	NM_005356	6.04
seryl-tRNA synthetase	NM_006513	6.04
v-src-1 Yamaguchi sarcoma viral related oncogene homolog	M79321	6.03
HSPC142 protein	BC006244	6.02
replication protein A1 (70kD)	NM_002945	5.99
ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	BG395660	5.98
membrane component, chromosome 11, surface marker 1	BG258784	5.96
H1 histone family, member X	NM_006026	5.95
Lysosomal-associated multispanning membrane protein-5	AI589086	5.95
PTD008 protein	NM_016145	5.95
poly(rC) binding protein 1	U24223	5.94
polyglutamine binding protein 1	AB041836	5.93
ariadne homolog 2 (Drosophila)	BC000422	5.93
MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B)	NM_005919	5.92
translocase of inner mitochondrial membrane 44 homolog (yeast)	NM_006351	5.92
intercellular adhesion molecule 2	NM_000873	5.91

FIG. 4C-8

bromodomain-containing 2	D42040	5.91
lysosomal-associated membrane protein 1	NM_005561	5.91
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1)	NM_005004	5.87
actin related protein 2/3 complex, subunit 2 (34 kD)	AF279893	5.84
Consensus includes gb:BG334495 /FEA=EST /DB_XREF=gi:13140933 /DB_XREF=est:602461128F1 /CLONE=IMAGE:4577718 /UG=Hs.228201 ESTs, Moderately similar to AF118094 25 PRO1992 H.sapiens	BG334495	5.84
isocitrate dehydrogenase 3 (NAD+) gamma	NM_004135	5.80
mitochondrial ribosomal protein L9	AB049636	5.80
transcription elongation factor B (SIII), polypeptide 2 (18kD, elongin B)	NM_007108	5.80
hypothetical protein	AI670847	5.80
HSPC274 protein	NM_014145	5.77
APEX nuclease (multifunctional DNA repair enzyme)	M80261	5.77
hematological and neurological expressed 1	NM_016185	5.75
hypothetical protein DKFZp434N185	NM_025205	5.75
eukaryotic translation initiation factor 4E-like 3	AF047695	5.75
N-acylaminoacyl-peptide hydrolase	NM_001640	5.74
KIAA0746 protein	AA522514	5.73
calpain, small subunit 1	AD001527	5.72
interleukin enhancer binding factor 3, 90kD	AF147209	5.69
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc-regulated)	NM_006773	5.67
hypothetical protein MGC10715	AL049650	5.67
chloride intracellular channel 1	AF034607	5.66
CD79B antigen (immunoglobulin-associated beta)	NM_000626	5.64
hydroxyacyl-Coenzyme A dehydrogenase, type II	NM_004493	5.64
zinc finger protein 207	BE871379	5.62
ribosomal protein S28	AC005011	5.61
syntaxin 16	AK026970	5.61
nuclear prelamin A recognition factor	NM_012336	5.61
cytochrome b-245, alpha polypeptide	NM_000101	5.60
actin related protein 2/3 complex, subunit 1A (41 kD)	NM_006409	5.60
mercaptopyruvate sulfurtransferase	NM_021126	5.57
Consensus includes gb:BF979419 /FEA=EST /DB_XREF=gi:12346634 /DB_XREF=est:602288246F1 /CLONE=IMAGE:4373914 /UG=Hs.119122 ribosomal protein L13a	BF979419	5.57
lymphocyte cytosolic protein 1 (L-plastin)	J02923	5.57
NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)	NM_004551	5.56
small nuclear ribonucleoprotein polypeptide A	NM_004596	5.55
pre-mRNA processing factor 31 homolog (yeast)	BF342707	5.55
protein phosphatase 1, catalytic subunit, alpha isoform	NM_002708	5.54
Tu translation elongation factor, mitochondrial	NM_003321	5.54
KIAA0618 gene product	AA514622	5.52

FIG. 4C-9

protein kinase, DNA-activated, catalytic polypeptide	U34994	5.51
Cw1 antigen	M12679	5.50
protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	NM_014225	5.49
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	NM_003406	5.49
guanine nucleotide binding protein (G protein), beta polypeptide 2	NM_005273	5.45
TAP binding protein (tapasin)	AF029750	5.43
solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	NM_002394	5.42
signal sequence receptor, beta (translocon-associated protein beta)	NM_003145	5.41
proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7)	U17496	5.36
RNB6	NM_016337	5.33
glutathione peroxidase 1	NM_000581	5.29
KIAA0123 protein	BF570122	5.28
flap structure-specific endonuclease 1	NM_004111	5.27
ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 21kD	BC005876	5.27
putative methyltransferase	NM_017528	5.27
RNA binding motif protein 5	U23946	5.26
GTP cyclohydrolase I feedback regulatory protein	NM_005258	5.25
H2A histone family, member O	AI313324	5.25
hypothetical protein R32184_1	BC001648	5.25
farnesyl-diphosphate farnesyltransferase 1	BC003573	5.25
glycoprotein, synaptic 2	NM_004868	5.22
peptidylprolyl isomerase E (cyclophilin E)	AF042386	5.21
FK506 binding protein 1A (12kD)	BC005147	5.19
guanine nucleotide binding protein (G protein), beta polypeptide 2- like 1	NM_006098	5.15
lymphocyte-specific protein tyrosine kinase	U07236	5.13
MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (<i>S. cerevisiae</i>)	NM_006739	5.12
homeo box A1	AC004079	5.11
HLA-B associated transcript 3	NM_004639	5.11
tubulin alpha 6	BC005946	5.10
endonuclease G	NM_004435	5.10
similar to RIKEN cDNA 2310040G17 gene	BF972185	5.09
protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	M18468	5.09
Consensus includes gb:BG531983 /FEA=EST /DB_XREF=gi:13523521 /DB_XREF=est:602561007F1 /CLONE=IMAGE:4699176 /UG=Hs.108104 ubiquitin-conjugating enzyme E2L 3 /FL=gb:NM_003347.1	BG531983	5.08
protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	BC000425	5.07
proteasome (prosome, macropain) subunit, beta type, 3	NM_002795	5.07
T cell receptor alpha locus	M12423	5.06

FIG. 4C-10

MCM7 minichromosome maintenance deficient 7 (<i>S. cerevisiae</i>)	D55716	5.06
nuclear distribution gene C (<i>A.nidulans</i>) homolog	AF241788	5.05
T cell receptor alpha locus	L34703	5.04
HLA-B associated transcript 3	BC003133	5.02
ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), member D	AL566172	5.00
actin, gamma 1	AU145192	4.99
kinesin-like 4	AC002301	4.98
karyopherin (importin) beta 3	NM_002271	4.98
translocase of inner mitochondrial membrane 10 homolog (yeast)	NM_012456	4.98
baculoviral IAP repeat-containing 5 (survivin)	AB028869	4.98
stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	AL553320	4.97
ribosomal protein, large, P1	NM_001003	4.97
myosin ID	AA621962	4.97
Xq28, 2000bp sequence contg. ORF	BE676218	4.96
GDP-mannose pyrophosphorylase A	NM_013335	4.96
casein kinase 2, beta polypeptide	NM_001320	4.91
proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	U51007	4.90
cullin 1	NM_003592	4.90
Huntingtin interacting protein B	AF049103	4.90
HLA-G histocompatibility antigen, class I, G	M90684	4.87
solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 5	AB018009	4.86
manic fringe homolog (<i>Drosophila</i>)	AI738965	4.85
RNA-binding protein (autoantigenic)	NM_016732	4.85
heat shock 70kD protein 4	BC002526	4.84
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1	AF231056	4.84
leucine rich repeat (in FLII) interacting protein 1	NM_004735	4.83
Rho GDP dissociation inhibitor (GDI) alpha	NM_004309	4.83
adaptor-related protein complex 2, sigma 1 subunit	BC006337	4.82
lymphotoxin beta (TNF superfamily, member 3)	NM_002341	4.81
cytochrome c oxidase subunit Vb	NM_001862	4.81
chromosome 11 open reading frame2	NM_013265	4.79
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (14.5kD, B14.5a)	NM_005001	4.78
KIAA0906 protein	AA502912	4.77
splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	NM_006924	4.77
CD37 antigen	NM_001774	4.77
tubulin alpha 6	BC004949	4.74
block of proliferation 1	BG491842	4.74
peroxiredoxin 1	L19184	4.73
thymopoietin	AF113682	4.72
cyclin-dependent kinase 4	NM_000075	4.71
ribosomal protein L13a	BC001675	4.70

FIG. 4C-11

T cell receptor alpha locus	M15565	4.69
PAI-1 mRNA-binding protein	BC003049	4.66
NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)	NM_002496	4.63
ribosomal protein L13a	BF942308	4.60
serine palmitoyltransferase, long chain base subunit 2	U15555	4.60
isopentenyl-diphosphate delta isomerase	BC005247	4.58
major histocompatibility complex, class II, DM alpha	X76775	4.57
flightless I homolog (Drosophila)	A1830227	4.57
translocating chain-associating membrane protein	NM_014294	4.56
H2A histone family, member X	NM_002105	4.55
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (8kD, AGGG)	NM_004546	4.55
transcriptional regulator protein	NM_013260	4.53
succinate dehydrogenase complex, subunit B, iron sulfur (lp)	NM_003000	4.52
Sjogren's syndrome/scleroderma autoantigen 1	NM_006396	4.51
RuvB-like 2 (E. coli)	NM_006666	4.49
major histocompatibility complex, class II, DQ alpha 1	BG397856	4.48
SH3-domain, GRB2-like, endophilin B2	NM_020145	4.47
hypothetical protein MGC4368	NM_024510	4.47
isopentenyl-diphosphate delta isomerase	NM_004508	4.47
ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	A1587323	4.46
Consensus includes gb:BF695847 /FEA=EST /DB_XREF=gi:11981255 /DB_XREF=est:601852205F1 /CLONE=IMAGE:4076232 /UG=Hs.301917 YDD19 protein	BF695847	4.45
Consensus includes gb:X02189 /DEF=H.sapiens adenosine deaminase (ADA) gene 5 flanking region and exon 1 (and joined CDS) /FEA=CDS /DB_XREF=gi:28358 /UG=Hs.1217 adenosine deaminase	X02189	4.44
insulin induced gene 1	BE300521	4.41
inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	D13889	4.40
eukaryotic translation elongation factor 1 gamma	NM_001404	4.40
Consensus includes gb:AJ011414.1 /DEF=Homo sapiens mRNA for plexin-B1 plasma membrane receptor, truncated splice variant (plexin-B1SEP gene). /FEA=mRNA /GEN=plexin-B1SEP /PROD=plexin-B1SEP receptor /DB_XREF=gi:5918164 /UG=Hs.312939 Homo sapiens mRNA for	AJ011414	4.40
chromosome condensation-related SMC-associated protein 1	AK022511	4.40
Consensus includes gb:BF530535 /FEA=EST /DB_XREF=gi:11617898 /DB_XREF=est:602071788F1 /CLONE=IMAGE:4214660 /UG=Hs.77665 KIAA0102 gene product /FL=gb:D14658.1 gb:NM_014752.1	BF530535	4.39
fuse-binding protein-interacting repressor	AF217197	4.38
mitochondrial carrier homolog 2	NM_014342	4.36
cytochrome c oxidase subunit VIIc	AA382702	4.36
v-raf-1 murine leukemia viral oncogene homolog 1	NM_002880	4.36

FIG. 4C-12

ribosomal protein L13a	NM_012423	4.35
potassium channel, subfamily K, member 12	NM_022055	4.35
polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I)	AA679988	4.34
DKFZP586M1523 protein	BF063896	4.34
KIAA0618 gene product	N29665	4.33
leucine-rich repeat protein, neuronal 1	AI654857	4.33
hypothetical protein FLJ20512	NM_017854	4.32
structure specific recognition protein 1	NM_003146	4.31
valyl-tRNA synthetase 2	NM_006295	4.30
RNA binding motif protein 4	NM_002896	4.30
KIAA0922 protein	AL136932	4.30
ribosomal protein, large P2	NM_001004	4.30
Consensus includes gb:AA653300 /FEA=EST /DB_XREF=gi:2589471 /DB_XREF=est:ag65c10.s1 /CLONE=IMAGE:1127826 /UG=Hs.132390 zinc finger protein 36 (KOX 18)	AA653300	4.29
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (19kD, PGIV)	NM_014222	4.27
golgi associated, gamma adaptin ear containing, ARF binding protein 2	BC000284	4.27
phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)	BE622627	4.26
HS1 binding protein	NM_006118	4.26
HSPC003 protein	NM_014017	4.25
KIAA0618 gene product	AI768378	4.25
dynactin 1 (p150, glued homolog, Drosophila)	NM_004082	4.25
cytosolic acyl coenzyme A thioester hydrolase	NM_007274	4.25
DnaJ (Hsp40) homolog, subfamily C, member 8	NM_014280	4.23
cold shock domain protein A	NM_003651	4.23
CDW52 antigen (CAMPATH-1 antigen)	N90866	4.20
hypothetical protein MGC2594	NM_024050	4.20
mitochondrial solute carrier	BE677761	4.20
ribonuclease H1	NM_002936	4.19
C2f protein	U72514	4.18
adaptor-related protein complex 2, sigma 1 subunit	NM_004069	4.18
hypothetical protein FLJ10359	NM_018072	4.17
branched chain aminotransferase 1, cytosolic	NM_005504	4.17
FK506 binding protein precursor	NM_016594	4.16
Consensus includes gb:AW582267 /FEA=EST /DB_XREF=gi:7257316 /DB_XREF=est:QV0-ST0215-060100-083- c06 /UG=Hs.306951 Human DNA sequence from clone RP11- 375F2 on chromosome 1 Contains a pseudogene similar to UBL1 (ubiquitin-like 1 (sentrin)), a pseudogene sim	AW582267	4.15
DKFZp434J1813 protein	BG168666	4.14
G-2 and S-phase expressed 1	BF305380	4.14
ribosomal protein L27a	NM_000990	4.14
neutrophil cytosolic factor 1 (47kD, chronic granulomatous	NM_000265	4.13

FIG. 4C-13

disease, autosomal 1)		
serum/glucocorticoid regulated kinase-like	NM_013257	4.13
FK506 binding protein 1A (12kD)	BC001002	4.13
phosphogluconate dehydrogenase	NM_002631	4.13
non-POU-domain-containing, octamer-binding	BC003129	4.12
RNA binding motif protein 10	AL137421	4.12
aspartyl aminopeptidase	NM_012100	4.12
tetraspan 3	NM_005724	4.12
Ewing sarcoma breakpoint region 1	BC000527	4.10
ret finger protein	AF230394	4.10
ribonuclease 6 precursor	NM_003730	4.09
tumor protein D52	BG389015	4.09
Consensus includes gb:BG537190 /FEA=EST		
/DB_XREF=gi:13528922 /DB_XREF=est:602565589F1		
/CLONE=IMAGE:4690079 /UG=Hs.111334 ferritin, light		
polypeptide	BG537190	4.08
BCL2-interacting killer (apoptosis-inducing)	NM_001197	4.08
KIAA0310 gene product	BC001404	4.07
accessory proteins BAP31/BAP29	NM_005745	4.06
proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	NM_002813	4.05
neutrophil cytosolic factor 1 (47kD, chronic granulomatous		
disease, autosomal 1)	AW072388	4.05
butyrophilin, subfamily 3, member A2	BC002832	4.04
B-cell associated protein	NM_007273	4.03
ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta		
polypeptide, 56/58kD, isoform 2	NM_001693	4.02
mitochondrial ribosomal protein S7	NM_015971	4.01
major histocompatibility complex, class I, E	NM_005516	4.00
mitogen-activated protein kinase kinase 3	AA780381	4.00
KIAA0699 protein	BC002327	3.99
protein phosphatase 1, regulatory subunit 7	NM_002712	3.99
KIAA0729 protein	AW502434	3.98
thyroid autoantigen 70kD (Ku antigen)	NM_001469	3.97
proteasome (prosome, macropain) subunit, beta type, 9 (large		
multifunctional protease 2)	NM_002800	3.97
hypothetical protein MGC5585	NM_024057	3.96
polymerase (RNA) II (DNA directed) polypeptide I (14.5kD)	AL037557	3.94
B-cell translocation gene 1, anti-proliferative	AL535380	3.94
hypothetical protein FLJ20859	NM_022734	3.93
ATP citrate lyase	U18197	3.92
GNAS complex locus	AF064092	3.92
gb:M24669.1 /DEF=Human Ig rearranged H-chain V-region mRNA		
(C-D-JH6), complete cds. /FEA=mRNA /GEN=IGH@		
/DB_XREF=gi:185200 /FL=gb:M24669.1	M24669	3.92
major histocompatibility complex, class I, E	M31183	3.91
insulin induced gene 1	NM_005542	3.91
Consensus includes gb:AI001784 /FEA=EST	AI001784	3.91

FIG. 4C-14

/DB_XREF=gi:3202255 /DB_XREF=est:ot41g06.s1		
/CLONE=IMAGE:1619386 /UG=Hs.308332 ESTs, Highly similar to		
A42735 ribosomal protein L10, cytosolic H.sapiens		
Consensus includes gb:Z82202 /DEF=Human DNA sequence		
from clone RP1-34P24 on chromosome 22 Contains a		
pseudogene similar to ribosomal protein L35, ESTs, STSs and		
GSSs /FEA=CDS /DB_XREF=gi:4107193 /UG=Hs.247778 Human		
DNA sequence from clone RP1-34P24 on c		
	Z82202	3.89
heterogeneous nuclear ribonucleoprotein R	NM_005826	3.89
platelet-activating factor acetylhydrolase, isoform Ib, gamma		
subunit (29kD)	NM_002573	3.89
hypothetical protein	BG257762	3.89
cytochrome c oxidase subunit Vb	BC006229	3.88
DKFZP547E1010 protein	AF261137	3.88
interferon regulatory factor 3	NM_001571	3.87
postmeiotic segregation increased 2-like 9	U38979	3.86
putative cyclin G1 interacting protein	NM_006349	3.86
GNAS complex locus	NM_000516	3.86
cyclin-dependent kinase 5	NM_004935	3.86
hippocalcin-like 1	NM_002149	3.86
24-dehydrocholesterol reductase	NM_014762	3.86
2',5'-oligoadenylate synthetase 1 (40-46 kD)	NM_002534	3.85
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 30	NM_014966	3.85
CREBBP/EP300 inhibitory protein 1	AF274951	3.85
adenylate kinase 2	U39945	3.84
structure specific recognition protein 1	BE795648	3.84
Rho GDP dissociation inhibitor (GDI) alpha	BC005851	3.84
Consensus includes gb:X04802 /DEF=Homo sapiens UBBP2		
pseudogene for ubiquitin UBB /FEA=CDS /DB_XREF=gi:37582		
/UG=Hs.247890 Homo sapiens UBBP2 pseudogene for ubiquitin		
UBB	X04802	3.84
ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	NM_003969	3.83
adenosine deaminase	NM_000022	3.83
kinesin 2 (60-70kD)	AA284075	3.82
eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)	NM_001415	3.82
hypothetical protein PRO1847	AF119855	3.82
enhancer of invasion 10	NM_021178	3.82
MCM2 minichromosome maintenance deficient 2, mitotin (S.		
cerevisiae)	NM_004526	3.81
CDC37 cell division cycle 37 homolog (S. cerevisiae)	U63131	3.81
WD repeat domain 1	AB010427	3.81
A kinase (PRKA) anchor protein 2	BE879367	3.81
neural precursor cell expressed, developmentally down-regulated		
8	NM_006156	3.80
olfactory receptor, family 1, subfamily K, member 1	NM_018835	3.80
GNAS complex locus	AF088184	3.79
translocase of inner mitochondrial membrane 23 homolog (yeast)	NM_006327	3.79
O-6-methylguanine-DNA methyltransferase	NM_002412	3.79

FIG. 4C-15

eukaryotic translation elongation factor 1 alpha 1	NM_001402	3.79
H3 histone, family 3B (H3.3B)	NM_005324	3.79
KIAA0974 protein	BE551340	3.78
S-adenosylmethionine decarboxylase 1	M21154	3.77
hypothetical protein MGC:5244,	NM_031213	3.76
nucleotide binding protein 2 (MinD homolog, E. coli)	NM_012225	3.75
cut-like 1, CCAAT displacement protein (Drosophila)	NM_001913	3.75
splicing factor 3a, subunit 3, 60kD	NM_006802	3.75
ribosomal protein S18	NM_022551	3.74
zinc finger protein 259	NM_003904	3.74
paired immunoglobulin-like receptor beta	NM_013440	3.73
serine/threonine kinase 15	NM_003600	3.73
chromosome 20 open reading frame 1	AF098158	3.73
SH3 domain binding glutamic acid-rich protein like 3	NM_031286	3.72
cyclin G2	L49506	3.72
ARP2 actin-related protein 2 homolog (yeast)	NM_005722	3.71
ubiquitin specific protease 7 (herpes virus-associated)	NM_003470	3.69
deoxyhypusine synthase	NM_001930	3.69
serologically defined colon cancer antigen 16	BC001149	3.69
ribosomal protein L10	AL031276	3.68
PRKC, apoptosis, WT1, regulator	AI336206	3.68
hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	U04627	3.67
gb:Z25433.1 /DEF=H.sapiens protein-serinethreonine kinase gene, complete CDS. /FEA=mRNA /PROD=protein- serinethreonine kinase /DB_XREF=gi:405744 /FL=gb:Z25433.1	Z25433	3.66
NRAS-related gene	AA167775	3.66
mesenchymal stem cell protein DSC92	NM_016645	3.65
SRY (sex determining region Y)-box 2	AW007161	3.65
chromatin-specific transcription elongation factor, 140 kDa subunit	NM_007192	3.65
uncoupling protein 2 (mitochondrial, proton carrier)	U82819	3.64
kinesin-like 6 (mitotic centromere-associated kinesin)	AY026505	3.63
lymphoid-restricted membrane protein	NM_006152	3.63
T-cell leukemia/lymphoma 1A	BC003574	3.63
ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD	NM_001695	3.63
chromatin assembly factor 1, subunit A (p150)	NM_005483	3.61
proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	NM_005789	3.60
KIAA1007 protein	BC000779	3.60
glia maturation factor, gamma	NM_004877	3.59
POP7 (processing of precursor, S. cerevisiae) homolog	BC001430	3.59
Breakpoint cluster region protein, uterine leiomyoma, 1; barrier to autointegration factor	AF044773	3.59
ubiquitin-like 5	NM_024292	3.59
hypothetical protein AF140225	NM_030799	3.58
NBR2	BC000924	3.58

FIG. 4C-16

deoxyhypusine synthase	U26266	3.58
peroxiredoxin 2	NM_005809	3.58
Consensus includes gb:BE731738 /FEA=EST /DB_XREF=gi:10145730 /DB_XREF=est:601568154F1 /CLONE=IMAGE:3842844 /UG=Hs.182937 peptidylprolyl		
isomerase A (cyclophilin A)	BE731738	3.58
sperm associated antigen 9	NM_003971	3.57
MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	AI859865	3.57
laminin receptor 1 (67kD, ribosomal protein SA)	AL136306	3.57
villin 2 (ezrin)	AA670344	3.57
zinc finger protein	NM_015871	3.57

FIG. 4D-1

Gene	NCBI Accession Number	FOLD DECREASE
ribosomal protein S11	BF680255	22.06
ribosomal protein, large P2	BC005354	15.91
Consensus includes gb:AJ249377.1 /DEF=Homo sapiens partial mRNA for human Ig lambda light chain variable region, clone MB91 (331 bp). /FEA=mRNA /GEN=IGLV /PROD=immunoglobulin lambda variable region /DB_XREF=gi:5911837 /UG=Hs.247898 Human anti-streptococ	AJ249377	15.77
calreticulin	AI378706	14.14
ribosomal protein S19	BC000023	14.00
Consensus includes gb:D84143.1 /DEF=Human immunoglobulin (mAb59) light chain V region mRNA, partial sequence. /FEA=mRNA /PROD=immunoglobulin light chain V-J region /DB_XREF=gi:1255613 /UG=Hs.121508 Human immunoglobulin (mAb59) light chain V region mRNA,	D84143	13.82
Consensus includes gb:AA292281 /FEA=EST /DB_XREF=gi:1940261 /DB_XREF=est:zt51b03.s1 /CLONE=IMAGE:725837 /UG=Hs.181307 H3 histone, family 3A	AA292281	13.65
ribosomal protein L27a	BE737027	13.26
Consensus includes gb:AW302047 /FEA=EST /DB_XREF=gi:6711724 /DB_XREF=est:xr52f08.x1 /CLONE=IMAGE:2763783 /UG=Hs.76230 ribosomal protein S10	AW302047	13.16
ribosomal protein S20	AF113008	10.69
Consensus includes gb:L48784 /DEF=050 Homo sapiens cDNA /FEA=mRNA /DB_XREF=gi:1066715 /UG=Hs.182426 ribosomal protein S2	L48784	8.01
J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	J04423	6.76
calreticulin	AA910371	6.64
Escherichia coli /REF=J04423 /DEF=E coli bioB gene biotin synthetase corresponding to nucleotides 2393-2682 of J04423 /LEN=1114 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	J04423	6.36
Cluster Incl. AI201594:qc02h12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1708487 /clone_end=3 /gb=AI201594 /gi=3754200 /ug=Hs.239333 /len=591	AI201594	6.20
ribosomal protein L27	BE312027	5.96
ribosomal protein L37a	BE857772	5.88
J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	J04423	5.80
Escherichia coli /REF=J04423 /DEF=E coli bioB gene biotin synthetase corresponding to nucleotides 2071-2304 of J04423 /LEN=1114 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	J04423	5.77

FIG. 4D-2

Escherichia coli /REF=J04423 /DEF=E coli bioB gene biotin synthetase corresponding to nucleotides 2772-3004 of J04423 /LEN=1114 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	J04423	5.72
J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	J04423	5.57
immunoglobulin lambda locus	AF043586	5.53
J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	J04423	5.35
ribosomal protein L38	AW303136	4.99
Consensus includes gb:AJ239383.1 /DEF=Homo sapiens mRNA for immunoglobulin heavy chain variable region, ID 31. /FEA=mRNA /GEN=IGHV /PROD=immunoglobulin heavy chain variable region /DB_XREF=gi:4456587 /UG=Hs.249245 Homo sapiens mRNA for single-chain anti	AJ239383	4.96
Consensus includes gb:AI345238 /FEA=EST /DB_XREF=gi:4082444 /DB_XREF=est:tb81b07.x1 /CLONE=IMAGE:2060725 /UG=Hs.111334 ferritin, light polypeptide	AI345238	4.95
Escherichia coli /REF=J04423 /DEF=E coli bioC protein corresponding to nucleotides 4257-4573 of J04423 /LEN=777 (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	J04423	4.76
hypothetical protein FLJ21034	NM_024940	4.69
Escherichia coli /REF=J04423 /DEF=E coli bioC protein corresponding to nucleotides 4609-4883 of J04423 /LEN=777 (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	J04423	4.64
ribosomal protein L38	BC000603	4.47
killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	X93596	4.39
PTPRF interacting protein, binding protein 1 (liprin beta 1)	N35896	4.31
hypothetical protein FLJ12619	BE465032	4.30
C-terminal binding protein 1	BF984434	4.29
Consensus includes gb:BF942161 /FEA=EST /DB_XREF=gi:12359481 /DB_XREF=est:nae87g10.x1 /CLONE=IMAGE:4118994 /UG=Hs.302797 ESTs	BF942161	4.27
Consensus includes gb:AF044592 /DEF=Homo sapiens lymphocyte-predominant Hodgkins disease case 4 immunoglobulin heavy chain gene, variable region, partial cds /FEA=CDS /DB_XREF=gi:2852420 /UG=Hs.248077 Homo sapiens lymphocyte-predominant Hodgkins disease	AF044592	4.24
hypothetical protein FLJ12985	NM_024924	4.24
thiopurine S-methyltransferase	U12387	4.22
J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	J04423	4.19
J04423 E coli bioC protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	J04423	4.17
Consensus includes gb:AL050122.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586E121 (from clone DKFZp586E121). /FEA=mRNA /DB_XREF=gi:4884330 /UG=Hs.274511 Homo sapiens mRNA;	AL050122	4.11

FIG. 4D-3

cDNA DKFZp586E121 (from clone DKFZp586E121)		
Consensus includes gb:AW301806 /FEA=EST		
/DB_XREF=gi:6711483 /DB_XREF=est:xr56e11.x1		
/CLONE=IMAGE:2764172 /UG=Hs.150551 ESTs, Weakly similar		
to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE		
CONTAMINATION WARNING ENTRY H.sapiens	AW301806	4.10
thromboxane A2 receptor	NM_001060	4.08
ADP-ribosylation factor 6	AA243143	4.02
PCTAIRE protein kinase 1	NM_006201	3.95
JTV1 gene	AF116615	3.90
hypothetical protein PRO1843	NM_018507	3.86
dystrophia myotonica-containing WD repeat motif	L19267	3.79
emopamil binding protein (sterol isomerase)	N58493	3.78
Escherichia coli /REF=J04423 /DEF=E coli bioD gene dethiobiotin		
synthetase corresponding to nucleotides 5312-5559 of J04423		
/LEN=676 (-5 and -3 represent transcript regions 5 prime and 3		
prime respectively)	J04423	3.77
Escherichia coli /REF=J04423 /DEF=E coli bioD gene dethiobiotin		
synthetase corresponding to nucleotides 5024-5244 of J04423		
/LEN=676 (-5 and -3 represent transcript regions 5 prime and 3		
prime respectively)	J04423	3.74
gb:AF090895.1 /DEF=Homo sapiens clone HQ0117 PRO0117		
mRNA, complete cds. /FEA=mRNA /PROD=PRO0117		
/DB_XREF=gi:6690166 /UG=Hs.283919 Homo sapiens clone		
HQ0117 PRO0117 mRNA, complete cds /FL=gb:AF090895.1	AF090895	3.71
GM2 ganglioside activator protein	X61094	3.70
putative protein O-mannosyltransferase	NM_013382	3.69
Consensus includes gb:BF973387 /FEA=EST		
/DB_XREF=gi:12340602 /DB_XREF=est:602242353F1		
/CLONE=IMAGE:4330861 /UG=Hs.305989 Human DNA		
sequence from clone RP3-483K16 on chromosome 6p12.1-21.1.		
Contains (parts of) two novel genes, RPS16 (40S Ribosomal		
protein	BF973387	3.69
M10098 Human 18S rRNA sequence, length 1969 bases, middle		
target bases 647-1292	M10098	3.69
aminopeptidase puromycin sensitive	BG153399	3.65
gb:Z25437.1 /DEF=H.sapiens protein-tyrosine kinase gene,		
complete CDS. /FEA=mRNA /PROD=protein-tyrosine kinase		
/DB_XREF=gi:405752 /FL=gb:Z25437.1	Z25437	3.63
Consensus includes gb:AK026825.1 /DEF=Homo sapiens cDNA:		
FLJ23172 fis, clone LNG10005. /FEA=mRNA		
/DB_XREF=gi:10439771 /UG=Hs.306885 Homo sapiens cDNA:		
FLJ23172 fis, clone LNG10005	AK026825	3.63
ubiquitously transcribed tetratricopeptide repeat gene, Y		
chromosome	NM_007125	3.61
Consensus includes gb:A1732770 /FEA=EST		
/DB_XREF=gi:5053883 /DB_XREF=est:zx78d05.x5		
/CLONE=IMAGE:809865 /UG=Hs.328688 ESTs, Moderately		
similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE		
CONTAMINATION WARNING ENTRY H.sapiens	A1732770	3.57

FIG. 4D-4

acidic epididymal glycoprotein-like 1	X95238	3.55
hypothetical protein FLJ10357	NM_018071	3.51
J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	J04423	3.48
Consensus includes gb:AV719355 /FEA=EST /DB_XREF=gi:10816507 /DB_XREF=est:AV719355 /CLONE=GLCEMB06 /UG=Hs.97109 ESTs	AV719355	3.44
KIAA1655 protein	AB051442	3.41
Consensus includes gb:AA890010 /FEA=EST /DB_XREF=gi:3016889 /DB_XREF=est:aj89h08.s1 /CLONE=IMAGE:1403679 /UG=Hs.50785 SEC22, vesicle trafficking protein (S. cerevisiae)-like 1	AA890010	3.41
hypothetical protein FLJ21603	NM_024762	3.41
protein kinase, interferon-inducible double stranded RNA dependent	NM_002759	3.40
hypothetical protein FLJ10298	NM_018050	3.40
translation initiation factor IF2	AB018284	3.39
collagen, type I, alpha 1	AI743621	3.39
alanine-glyoxylate aminotransferase 2-like 1	NM_031279	3.37
PRO0478 protein	NM_014129	3.36
Consensus includes gb:AW971134 /FEA=EST /DB_XREF=gi:8160979 /DB_XREF=est:EST383221 /UG=Hs.292245 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens	AW971134	3.32
sialophorin (gpL115, leukosialin, CD43)	NM_003123	3.31
islet cell autoantigen 1 (69kD)	BC005922	3.30
ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD)	NM_005177	3.30
protein phosphatase 2 (formerly 2A), regulatory subunit B" (PR 72), alpha isoform and (PR 130), beta isoform	AI760130	3.29
HIV-1 rev binding protein 2	AI912583	3.28
sorting nexin 4	AA524345	3.26
aldehyde dehydrogenase 1 family, member B1	BC001619	3.26
Consensus includes gb:AW971415 /FEA=EST /DB_XREF=gi:8161260 /DB_XREF=est:EST383504 /UG=Hs.165337 ESTs	AW971415	3.25
Consensus includes gb:AK026484.1 /DEF=Homo sapiens cDNA: FLJ22831 fis, clone KAIA4161. /FEA=mRNA /DB_XREF=gi:10439356 /UG=Hs.321666 Homo sapiens cDNA: FLJ22831 fis, clone KAIA4161	AK026484	3.25
G protein-coupled receptor 37 (endothelin receptor type B-like)	T16257	3.24
hypothetical protein FLJ14107	NM_025026	3.22
endomucin-1	NM_016241	3.22
pregnancy specific beta-1-glycoprotein 11	NM_002785	3.22
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	AA502643	3.21
Consensus includes gb:AI701156 /FEA=EST /DB_XREF=gi:4989056 /DB_XREF=est:we10f09.x1	AI701156	3.20

FIG. 4D-5

/CLONE=IMAGE:2340713 /UG=Hs.6580 Homo sapiens cDNA: FLJ23227 fis, clone CAE00645, highly similar to AF052138 Homo sapiens clone 23718 mRNA sequence Consensus includes gb:AK022473.1 /DEF=Homo sapiens cDNA FLJ12411 fis, clone MAMMA1002964. /FEA=mRNA /DB_XREF=gi:10433882 /UG=Hs.296722 Homo sapiens cDNA FLJ12411 fis, clone MAMMA1002964			AK022473	3.18
CDC5 cell division cycle 5-like (S. pombe) Consensus includes gb:BF573849 /FEA=EST /DB_XREF=gi:11647561 /DB_XREF=est:602132053F1 /CLONE=IMAGE:4271340 /UG=Hs.96343 ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! H.sapiens			AB007892	3.17
harakiri, BCL2 interacting protein (contains only BH3 domain)			BF573849	3.17
cytochrome P450 isoform 4F12			U76376	3.17
gb:BC006361.1 /DEF=Homo sapiens, clone MGC:13137, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:13137) /DB_XREF=gi:13623508 /FL=gb:BC006361.1			NM_023944	3.17
hypothetical protein FLJ22965			BC006361	3.16
Consensus includes gb:AF222691.1 /DEF=Homo sapiens Alu repeat (LNX1) mRNA sequence. /FEA=mRNA /DB_XREF=gi:12655850 /UG=Hs.307008 Homo sapiens Alu repeat (LNX1) mRNA sequence			NM_022101	3.15
clone FLB3816			AF222691	3.15
Consensus includes gb:AI524687 /FEA=EST /DB_XREF=gi:4438822 /DB_XREF=est:th12a07.x1 /CLONE=IMAGE:2118036 /UG=Hs.57969 phenylalanine-tRNA synthetase			NM_016415	3.15
hypothetical protein FLJ20897			AI524687	3.14
PI-3-kinase-related kinase SMG-1			AI335509	3.12
Consensus includes gb:AI683552 /FEA=EST /DB_XREF=gi:4893734 /DB_XREF=est:tx67h02.x1 /CLONE=IMAGE:2274675 /UG=Hs.201605 ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens			BE000837	3.11
KIAA0729 protein			AI683552	3.08
KIAA1827 protein			AK023845	3.07
C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 6			AW474158	3.07
SCAN domain-containing 2			AF200738	3.04
thyroid hormone receptor-associated protein, 95-kD subunit			AF244812	3.03
Consensus includes gb:AK024108.1 /DEF=Homo sapiens cDNA FLJ14046 fis, clone HEMBA1006461. /FEA=mRNA /DB_XREF=gi:10436406 /UG=Hs.142677 Homo sapiens cDNA FLJ14046 fis, clone HEMBA1006461			BG339606	3.02
tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcription factor IIIA-interacting protein			AK024108	3.02
Consensus includes gb:BG290532 /FEA=EST /DB_XREF=gi:13047560 /DB_XREF=est:602388395F1			NM_021980	3.02
			BG290532	3.01

FIG. 4D-6

/CLONE=IMAGE:4517206 /UG=Hs.11210 ESTs, Moderately similar to Z137_HUMAN ZINC FINGER PROTEIN 13 H.sapiens mitochondrial ribosomal protein S12	R68573	3.00
P3ECSL	NM_022164	2.99
lymphoid blast crisis oncogene	AF127481	2.99
KIAA0653 protein, B7-like protein	AF289028	2.99
Consensus includes gb:AF035317.1 /DEF=Homo sapiens clone 23892 mRNA sequence. /FEA=mRNA /DB_XREF=gi:2661080 /UG=Hs.91916 Homo sapiens clone 23892 mRNA sequence	AF035317	2.99
early lymphoid activation protein	L22650	2.98
lipopolysaccharide specific response-68 protein	NM_018678	2.97
tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	J03225	2.96
Consensus includes gb:AI734156 /FEA=EST /DB_XREF=gi:5055269 /DB_XREF=est:nc79d04.y5 /CLONE=IMAGE:783559 /UG=Hs.172895 ESTs	AI734156	2.96
Consensus includes gb:AW301937 /FEA=EST /DB_XREF=gi:6711614 /DB_XREF=est:xr85b03.x1 /CLONE=IMAGE:2766893 /UG=Hs.138036 ESTs	AW301937	2.95
immunoglobulin heavy constant mu	S55735	2.93
Consensus includes gb:X78262.1 /DEF=H.sapiens mRNA for TRE5. /FEA=mRNA /DB_XREF=gi:587440 /UG=Hs.302178 H.sapiens mRNA for TRE5	X78262	2.92
Consensus includes gb:R06655 /FEA=EST /DB_XREF=gi:757275 /DB_XREF=est:yf10e02.r1 /CLONE=IMAGE:126458 /UG=Hs.188518 ESTs, Moderately similar to AF078844 1 hqp0376 protein H.sapiens	R06655	2.91
somatostatin receptor 4	NM_001052	2.91
Consensus includes gb:AL163202 /DEF=Homo sapiens chromosome 21 segment HS21C002 /FEA=CDS /DB_XREF=gi:7717242 /UG=Hs.289121 Homo sapiens chromosome 21 segment HS21C002	AL163202	2.91
guanine nucleotide exchange factor for Rap1; M-Ras-regulated GEF	AI263837	2.90
hypothetical protein PRO0082	NM_018590	2.89
cathepsin S	BC002642	2.88
transducin (beta)-like 1	AA724134	2.88
Consensus includes gb:AK022303.1 /DEF=Homo sapiens cDNA FLJ12241 fis, clone MAMMA1001274. /FEA=mRNA /DB_XREF=gi:10433670 /UG=Hs.287503 Homo sapiens cDNA FLJ12241 fis, clone MAMMA1001274	AK022303	2.87
MAD, mothers against decapentaplegic homolog (Drosophila) interacting protein, receptor activation anchor	NM_007323	2.87
Consensus includes gb:AL050065.1 /DEF=Homo sapiens mRNA; cDNA DKFZp566M043 (from clone DKFZp566M043). /FEA=mRNA /DB_XREF=gi:4884295 /UG=Hs.212587 Homo sapiens mRNA; cDNA DKFZp566M043 (from clone DKFZp566M043)	AL050065	2.86
E74-like factor 4 (ets domain transcription factor)	NM_001421	2.85
hypothetical protein 384D8_6	BC000473	2.84

FIG. 4D-7

phosphodiesterase 10A	AF127480	2.84
PABP-interacting protein 2	AL043487	2.84
PRO1880 protein	NM_014104	2.83
serine protease inhibitor-like, with Kunitz and WAP domains 1 (eppin)	NM_020398	2.82
zinc finger protein 43 (HTF6)	AK022905	2.82
solute carrier family 4, sodium bicarbonate cotransporter, member 4	AF011390	2.82
rab3 GTPase-activating protein, non-catalytic subunit (150kD)	AK021928	2.81
carboxypeptidase N, polypeptide 2, 83kD	J05158	2.79
hypothetical protein FLJ12151	AK022213	2.79
neuronal thread protein	NM_014486	2.78
Consensus includes gb:AK021505.1 /DEF=Homo sapiens cDNA FLJ11443 fis, clone HEMBA1001330. /FEA=mRNA /DB_XREF=gi:10432701 /UG=Hs.297945 Homo sapiens cDNA FLJ11443 fis, clone HEMBA1001330	AK021505	2.78
KIAA0889 protein	NM_015377	2.78
coactivator-associated arginine methyltransferase-1	AL529396	2.77
ribonuclease P, 40kD subunit	NM_006638	2.76
solute carrier family 21 (organic anion transporter), member 6	AB026257	2.75
putative N6-DNA-methyltransferase	NM_013240	2.75
Consensus includes gb:AL080160.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434M054 (from clone DKFZp434M054). /FEA=mRNA /DB_XREF=gi:5262622 /UG=Hs.274517 Homo sapiens mRNA; cDNA DKFZp434M054 (from clone DKFZp434M054)	AL080160	2.74
dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease)	NM_001918	2.73
transforming, acidic coiled-coil containing protein 2	AF220152	2.73
prostate derived STE20-like kinase PSK	NM_016151	2.73
Consensus includes gb:AL157484.1 /DEF=Homo sapiens mRNA; cDNA DKFZp762M127 (from clone DKFZp762M127). /FEA=mRNA /DB_XREF=gi:7018527 /UG=Hs.22483 Homo sapiens mRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)	AL157484	2.73
dynamin 2	AK023207	2.73
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	NM_006080	2.72
G protein-coupled receptor kinase 6	BG423052	2.72
S100 calcium binding protein A11 (calgizzarin)	NM_005620	2.72
cytochrome c oxidase subunit Vb	AI557312	2.72
Epstein-Barr virus induced gene 3	NM_005755	2.71
Consensus includes gb:AW974816 /FEA=EST /DB_XREF=gi:8166019 /DB_XREF=est:EST386921 /UG=Hs.283517 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens	AW974816	2.71
bone morphogenetic protein receptor, type IB	D89675	2.71

FIG. 4D-8

prefoldin 4	NM_002623	2.70
hypothetical protein FLJ21032	NM_024906	2.70
glioma pathogenesis-related protein	U16307	2.70
epithelial membrane protein 3	NM_001425	2.69
Consensus includes gb:AK024958.1 /DEF=Homo sapiens cDNA: FLJ21305 fis, clone COL02124. /FEA=mRNA /DB_XREF=gi:10437382 /UG=Hs.287658 Homo sapiens cDNA: FLJ21305 fis, clone COL02124		
	AK024958	2.69
KRAB zinc finger protein KR18	AK024789	2.69
putative 28 kDa protein	AF349314	2.68
apolipoprotein L, 2	BC004395	2.68
Consensus includes gb:AL110201.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586F1622 (from clone DKFZp586F1622). /FEA=mRNA /DB_XREF=gi:5817120 /UG=Hs.278435 Homo sapiens mRNA; cDNA DKFZp586F1622 (from clone DKFZp586F1622)		
	AL110201	2.67
Consensus includes gb:R33964 /FEA=EST /DB_XREF=gi:789822 /DB_XREF=est:yh74c03.r1 /CLONE=IMAGE:135460 /UG=Hs.288681 Homo sapiens cDNA FLJ11022 fis, clone PLACE1003771		
	R33964	2.67
Consensus includes gb:AL137378.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434K1126 (from clone DKFZp434K1126). /FEA=mRNA /DB_XREF=gi:6807908 /UG=Hs.306455 Homo sapiens mRNA; cDNA DKFZp434K1126 (from clone DKFZp434K1126)		
	AL137378	2.67
translation initiation factor IF2	BG261322	2.67
KIAA1045 protein	AB028968	2.66
hypothetical protein	NM_019069	2.66
hypothetical protein FLJ23185	NM_025056	2.66
gamma-aminobutyric acid (GABA) A receptor, alpha 5	BF966183	2.66
colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	L29349	2.66
N-myristoyltransferase 2	NM_004808	2.64
JM27 protein	NM_007003	2.64
Consensus includes gb:AK023911.1 /DEF=Homo sapiens cDNA FLJ13849 fis, clone THYRO1000865. /FEA=mRNA /DB_XREF=gi:10435992 /UG=Hs.181810 Homo sapiens cDNA FLJ13849 fis, clone THYRO1000865		
	AK023911	2.63
immunoglobulin heavy constant mu	S74639	2.63
gb:NM_024305.1 /DEF=Homo sapiens hypothetical protein MGC4278 (MGC4278), mRNA. /FEA=mRNA /GEN=MGC4278 /PROD=hypothetical protein MGC4278 /DB_XREF=gi:13236535 /UG=Hs.318780 hypothetical protein MGC4278. /FL=gb:BC002659.1 gb:NM_024305.1		
	NM_024305	2.63
hypothetical protein MGC2474	NM_023931	2.62
hypothetical protein FLJ21477	NM_025153	2.62
polymerase (DNA directed), eta	NM_006502	2.62
Consensus includes gb:AI126492 /FEA=EST /DB_XREF=gi:3595006 /DB_XREF=est:qd82h06.x1 /CLONE=IMAGE:1736027 /UG=Hs.104258 Homo sapiens mRNA, AI126492		
	AI126492	2.62

FIG. 4D-9

exon 1, 2, 3, 4, clone:RES4-24A		
Consensus includes gb:BC005365.1 /DEF=Homo sapiens, clone		
IMAGE:3829438, mRNA, partial cds. /FEA=mRNA		
/PROD=Unknown (protein for IMAGE:3829438)		
/DB_XREF=gi:13529199 /UG=Hs.331237 Homo sapiens, clone		
IMAGE:3829438, mRNA, partial cds	BC005365	2.61
polymerase (RNA) II (DNA directed) polypeptide B (140kD)	AW770896	2.61
cAMP responsive element binding protein-like 1	U52696	2.61
neuropeptide Y receptor Y6 (pseudogene)	U59431	2.60
hexokinase 2	AI761561	2.60
Cluster Incl. AI949010:wq36a07.x1 Homo sapiens cDNA, 3 end		
/clone=IMAGE-2473332 /clone_end=3 /gb=AI949010 /gi=5741320		
/ug=Hs.104036 /len=457	AI949010	2.59
mannan-binding lectin serine protease 1 (C4/C2 activating		
component of Ra-reactive factor)	BC000587	2.59
SH3-domain GRB2-like 3	AF036269	2.59
thyroid hormone receptor interactor 11	BC002656	2.59
hypothetical protein PRO2849	NM_022335	2.58
decay accelerating factor for complement (CD55, Cromer blood		
group system)	BC001288	2.58
mitogen-activated protein kinase kinase 5	U71088	2.58
cofactor required for Sp1 transcriptional activation, subunit 2		
(150kD)	AK023368	2.57
phosphatidylinositol 4-kinase, catalytic, beta polypeptide	U81802	2.56
HCF-binding transcription factor Zhangfei	AI206560	2.56
kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen		
(R2 leukocyte antigen, antigen detected by monoclonal and		
antibody IA4))	NM_002231	2.56
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD)	NM_030881	2.55
RAP2B, member of RAS oncogene family	NM_002886	2.55
eukaryotic translation initiation factor 4 gamma, 1	BE966878	2.54
KIAA0472 protein	AB007941	2.54
isocitrate dehydrogenase 1 (NADP+), soluble	NM_005896	2.54
CED-6 protein	AK023668	2.53
ATP-binding cassette, sub-family D (ALD), member 3	NM_002858	2.53
eukaryotic translation initiation factor 5A	AA393940	2.53
glycophorin E	NM_002102	2.53
artemis protein	NM_022487	2.52
inhibin, beta C	NM_005538	2.52
reversion-inducing-cysteine-rich protein with kazal motifs	AK022897	2.52
Consensus includes gb:AU147017 /FEA=EST		
/DB_XREF=gi:11008538 /DB_XREF=est:AU147017		
/CLONE=HEMBB1002152 /UG=Hs.301905 Homo sapiens cDNA		
FLJ14080 fis, clone HEMBB1002152	AU147017	2.52
Mediterranean fever	NM_000243	2.52
hypothetical protein FLJ20837	NM_017964	2.52
Consensus includes gb:AL049260.1 /DEF=Homo sapiens mRNA;		
cDNA DKFZp564E233 (from clone DKFZp564E233). /FEA=mRNA	AL049260	2.51

FIG. 4D-10

/DB_XREF=gi:4500007 /UG=Hs.302050 Homo sapiens mRNA; cDNA DKFZp564E233 (from clone DKFZp564E233) Consensus includes gb:AK025724.1 /DEF=Homo sapiens cDNA: FLJ22071 fis, clone HEP11691. /FEA=mRNA /DB_XREF=gi:10438333 /UG=Hs.326248 Homo sapiens cDNA: FLJ22071 fis, clone HEP11691			AK025724	2.51
coagulation factor V (proaccelerin, labile factor)			NM_000130	2.49
ring finger protein 2			NM_007212	2.49
ATPase, Class I, type 8B, member 1			BG252666	2.49
homeo box A10			AI375919	2.49
Consensus includes gb:AF043583.1 /DEF=Homo sapiens clone ASMneg1-b3 immunoglobulin lambda chain VJ region, (IGL) mRNA, partial cds. /FEA=mRNA /GEN=IGL /PROD=immunoglobulin lambda chain /DB_XREF=gi:2865477 /UG=Hs.248083 Homo sapiens clone ASMneg1-b3 immu			AF043583	2.49
nucleolar protein 4			NM_003787	2.48
macrophage stimulating, pseudogene 9			U28055	2.48
death-associated protein kinase 2			AK026801	2.48
ubiquitin specific protease 15			AF106069	2.48
Consensus includes gb:AW301806 /FEA=EST /DB_XREF=gi:6711483 /DB_XREF=est:xr56e11.x1 /CLONE=IMAGE:2764172 /UG=Hs.150551 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens			AW301806	2.47
Fc fragment of IgG, low affinity IIIb, receptor for (CD16)			J04162	2.47
Consensus includes gb:U43604.1 /DEF=Human unidentified mRNA, partial sequence. /FEA=mRNA /DB_XREF=gi:1171236 /UG=Hs.159901 Human unidentified mRNA, partial sequence			U43604	2.47
prostate differentiation factor			AF003934	2.47
X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)			X03453	2.47
protein kinase, cAMP-dependent, regulatory, type II, alpha			BC002763	2.47
hypothetical protein FLJ10534			AK026565	2.46
Consensus includes gb:AW574933 /FEA=EST /DB_XREF=gi:7246472 /DB_XREF=est:UI-HF-BL0-abq-b-09-0- UI.s1 /CLONE=IMAGE:3057353 /UG=Hs.248844 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens			AW574933	2.46
nerve growth factor receptor (TNFR superfamily, member 16)			NM_002507	2.46
neuropilin 2			AA295257	2.46
erythrocyte membrane protein band 7.2 (stomatin)			AI537887	2.46
ladinin 1			U58994	2.46
Consensus includes gb:AK026493.1 /DEF=Homo sapiens cDNA: FLJ22840 fis, clone KAIA4709. /FEA=mRNA /DB_XREF=gi:10439366 /UG=Hs.287293 Homo sapiens cDNA: FLJ22840 fis, clone KAIA4709			AK026493	2.45
heterogeneous nuclear ribonucleoprotein H1 (H)			AV753392	2.45
adducin 2 (beta)			NM_017482	2.45
zinc finger protein 76 (expressed in testis)			NM_003427	2.45

FIG. 4D-11

Consensus includes gb:BE672313 /FEA=EST		
/DB_XREF=gi:10032854 /DB_XREF=est:7a59b10.x1		
/CLONE=IMAGE:3223003 /UG=Hs.34054 Homo sapiens cDNA:		
FLJ22488 fis, clone HRC10948, highly similar to HSU79298		
Human clone 23803 mRNA	BE672313	2.45
dimethylarginine dimethylaminohydrolase 1	AL078459	2.44
PRO0644 protein	NM_014136	2.44
coat protein gamma-cop	NM_016128	2.43
Consensus includes gb:BG403790 /FEA=EST		
/DB_XREF=gi:13297238 /DB_XREF=est:602419627F1		
/CLONE=IMAGE:4526599 /UG=Hs.158154 ESTs	BG403790	2.43
sema domain, immunoglobulin domain (Ig), short basic domain,		
secreted, (semaphorin) 3C	NM_006379	2.43
UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide		
5	NM_006057	2.42
hypothetical protein FLJ20059	NM_017644	2.42
CDC14 cell division cycle 14 homolog A (S. cerevisiae)	NM_003672	2.41
hypothetical protein FLJ23548	NM_024590	2.41
hypothetical protein FLJ22558	NM_022747	2.41
nuclear factor I/B	U70862	2.40
hypothetical protein My014	NM_030918	2.40
hypothetical protein FLJ20006	NM_017618	2.40
WNT1 inducible signaling pathway protein 3	AF143679	2.40
dickkopf homolog 2 (Xenopus laevis)	NM_014421	2.39
Consensus includes gb:AK021440.1 /DEF=Homo sapiens cDNA		
FLJ11378 fis, clone HEMBA1000456. /FEA=mRNA		
/DB_XREF=gi:10432625 /UG=Hs.6937 hypothetical protein		
FLJ10276	AK021440	2.39
Consensus includes gb:AL359578.1 /DEF=Homo sapiens mRNA;		
cDNA DKFZp547N163 (from clone DKFZp547N163). /FEA=mRNA		
/DB_XREF=gi:8655637 /UG=Hs.306511 Homo sapiens mRNA;		
cDNA DKFZp547N163 (from clone DKFZp547N163)	AL359578	2.39
Consensus includes gb:AA629050 /FEA=EST		
/DB_XREF=gi:2541437 /DB_XREF=est:zu84a06.s1		
/CLONE=IMAGE:744658 /UG=Hs.50760 ESTs, Highly similar to		
BimL H.sapiens	AA629050	2.39
Dystonia musculorum of mouse, human homolog of	AL049215	2.39
Consensus includes gb:AF131777.1 /DEF=Homo sapiens clone		
25061 mRNA sequence. /FEA=mRNA /DB_XREF=gi:4406602		
/UG=Hs.183475 Homo sapiens clone 25061 mRNA sequence	AF131777	2.39
hypothetical protein FLJ22746	NM_024785	2.38
H1 histone family, member 4	AL353759	2.38
unc-51-like kinase 2 (C. elegans)	BG526973	2.38
zinc finger protein 42 (myeloid-specific retinoic acid- responsive)	AI733248	2.38
checkpoint suppressor 1	AA860806	2.37
protease, serine, 21 (testisin)	NM_006799	2.37
peptidyl arginine deiminase, type V	AF229067	2.37
calpain 9 (nCL-4)	AB038463	2.37
sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3	L25275	2.37

FIG. 4D-12

EphB3	X75208	2.37
craniofacial development protein 1	D85939	2.36
sialophorin (gpL115, leukosialin, CD43)	X60502	2.36
Consensus includes gb:K00627.1 /DEF=human kpni repeat mrna (cdna clone pcd-kpni-8), 3 end. /FEA=mRNA /DB_XREF=gi:337653 /UG=Hs.203776 Human kpni repeat mrna (cdna clone pcd-kpni-8), 3 end	K00627	2.36
Consensus includes gb:AK022045.1 /DEF=Homo sapiens cDNA FLJ11983 fis, clone HEMBB1001337. /FEA=mRNA /DB_XREF=gi:10433364 /UG=Hs.193162 Homo sapiens cDNA FLJ11983 fis, clone HEMBB1001337	AK022045	2.36
hypothetical protein FLJ20097	NM_017667	2.36
Consensus includes gb:M78162 /FEA=EST /DB_XREF=gi:273899 /DB_XREF=est:EST01755 /CLONE=HHCPN60 /UG=Hs.314534 ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens	M78162	2.35
hypothetical protein FLJ20019	NM_017624	2.35
calcium/calmodulin-dependent serine protein kinase (MAGUK family)	AB039327	2.35
M10098 Human 18S rRNA gene, complete (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	M10098	2.35
Consensus includes gb:S80491.1 /DEF=stem cell factor {alternatively spliced} human, preimplantation embryos, blastocysts, mRNA Partial, 180 nt. /FEA=mRNA /GEN=stem cell factor, SCF /PROD=stem cell factor /DB_XREF=gi:1246099 /UG=Hs.123028 Stem cell facto	S80491	2.35
hemoglobin, gamma G	NM_000184	2.34
transcription factor 20 (AR1)	U19345	2.34
Consensus includes gb:AK023783.1 /DEF=Homo sapiens cDNA FLJ13721 fis, clone PLACE2000450. /FEA=mRNA /DB_XREF=gi:10435820 /UG=Hs.289035 Homo sapiens cDNA FLJ13721 fis, clone PLACE2000450	AK023783	2.34
CGI-58 protein	NM_016006	2.34
hypothetical protein FLJ10254	NM_018041	2.34
interleukin 1 receptor antagonist	BE563442	2.33
Bloom syndrome	NM_000057	2.33
Consensus includes gb:AA780524 /FEA=EST /DB_XREF=gi:2839855 /DB_XREF=est:ac71f01.s1 /CLONE=IMAGE:868057 /UG=Hs.294072 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens	AA780524	2.33
potassium inwardly-rectifying channel, subfamily J, member 8	NM_004982	2.33
hypothetical protein FLJ14310	NM_025028	2.33
thrombospondin 1	NM_003246	2.33
calmodulin 1 (phosphorylase kinase, delta)	M27319	2.32
leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	AF009643	2.32
M10098 Human 18S rRNA sequence, length 1969 bases, 3 prime target bases 1293-1938	M10098	2.32
hypothetical protein FLJ23447	NM_024825	2.32

FIG. 4D-13

KIAA0304 gene product	AF105279	2.32
a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	NM_003183	2.32
SRY (sex determining region Y)-box 21	NM_007084	2.32
phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	NM_005028	2.32
homeo box C8	NM_022658	2.32
CGI-86 protein	BC000637	2.32
guanine nucleotide binding protein 13, gamma	NM_016541	2.31
potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	NM_002252	2.31
Consensus includes gb:AK000864.1 /DEF=Homo sapiens cDNA FLJ10002 fis, clone HEMBA1000046. /FEA=mRNA		
/DB_XREF=gi:7021188 /UG=Hs.296522 Homo sapiens cDNA FLJ10002 fis, clone HEMBA1000046	AK000864	2.31
nuclear LIM interactor-interacting factor	AF229163	2.31
Consensus includes gb:AW451711 /FEA=EST		
/DB_XREF=gi:6992487 /DB_XREF=est:UI-H-BI3-ale-c-02-0-UI.s1		
/CLONE=IMAGE:2736386 /UG=Hs.313760 ESTs	AW451711	2.31
Consensus includes gb:AW090043 /FEA=EST		
/DB_XREF=gi:6047387 /DB_XREF=est:xd01c05.x1		
/CLONE=IMAGE:2592488 /UG=Hs.326464 Homo sapiens cDNA: FLJ21702 fis, clone COL09874	AW090043	2.31
elaC homolog 1 (E. coli)	NM_018696	2.31